

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:38:20 ; Search time 89.6501 Seconds
(without alignments)
1488.535 Million cell updates/sec

Title: US-10-070-532-6

Perfect score: 1947

Sequence: 1 MEPSATPGAQMGVPPGSREP.....ANPIIYNFLSGCCKEKSILVLS 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1947	100.0	372	4	AAU00440	Aau00440 Human neu
2	1944	99.8	377	2	AAW06126	Aaw06126 Neuropept
3	1943	99.8	389	2	AAW80805	Aaw80805 Amino aci
4	1943	99.8	389	4	AAU11187	Aau11187 Human G p
5	1943	99.8	389	5	ABB08208	Abb08208 G-protein
6	1903	97.7	369	2	AAW06125	Aaw06125 Neuropept
7	1903	97.7	425	2	AAW80456	Aaw80456 G-protein
8	1903	97.7	425	4	AAU11188	Aau11188 Human G p
9	1903	97.7	425	4	AAU11186	Aau11186 Human G p

10	1903	97.7	425	4	AAB67079	Aab67079 Human HFG
11	1903	97.7	425	5	AAG78345	Aag78345 Human HFG
12	1903	97.7	425	6	ABP81941	Abp81941 Human ore
13	1903	97.7	425	7	ABG75058	Abg75058 Human ore
14	1903	97.7	425	7	ADK52564	Adk52564 Hematolog
15	1903	97.7	425	8	ADL22443	Adl22443 Human ore
16	1903	97.7	425	8	ADL22428	Adl22428 Human ore
17	1903	97.7	425	8	ADO29106	Ado29106 Human nov
18	1898	97.5	425	4	ABB56378	Abb56378 Non-endog
19	1897	97.4	425	4	AAU00438	Aau00438 Human neu
20	1897	97.4	425	4	AAB67489	Aab67489 Amino aci
21	1896	97.4	402	2	AAW06124	Aaw06124 Neuropept
22	1886.5	96.9	401	5	AAG78346	Aag78346 Human HFG
23	1875	96.3	369	4	AAU00439	Aau00439 Human neu
24	1870	96.0	425	4	AAE04740	Aae04740 Cynomolgo
25	1810	93.0	364	4	AAU00442	Aau00442 Human neu
26	1785	91.7	416	8	ADO29107	Ado29107 Mouse nov
27	1783	91.6	427	4	AAB47300	Aab47300 Dog orexi
28	1347.5	69.2	444	4	AAB61968	Aab61968 Canine wi
29	1344.5	69.1	444	4	AAB84416	Aab84416 Amino aci
30	1343.5	69.0	443	8	ADO29110	Ado29110 Mouse nov
31	1342.5	69.0	460	4	AAB61970	Aab61970 Rat HCCTR
32	1342.5	69.0	460	6	ABG73515	Abg73515 Rat OX2R
33	1341.5	68.9	444	4	AAB98007	Aab98007 Human hyp
34	1341.5	68.9	444	4	AAB61969	Aab61969 Human HCR
35	1341.5	68.9	444	6	ABG73514	Abg73514 Human OX2
36	1341.5	68.9	444	6	ABP81942	Abp81942 Human ore
37	1341.5	68.9	444	7	ABG75059	Abg75059 Human ore
38	1341.5	68.9	444	8	ADO29109	Ado29109 Human nov
39	1340.5	68.8	444	2	AAY03649	Aay03649 Human 7-t
40	1336.5	68.6	444	4	ABB56379	Abb56379 Non-endog
41	1307	67.1	263	2	AAR91233	Aar91233 Rabbit G-
42	1307	67.1	263	2	AAW11236	Aaw11236 G-protein
43	1161.5	59.7	330	4	AAB61971	Aab61971 Canine na
44	994	51.1	327	4	AAB61972	Aab61972 Canine na
45	495.5	25.4	430	8	ADJ87508	Adj87508 Murine re

ALIGNMENTS

RESULT 1

AAU00440

ID AAU00440 standard; protein; 372 AA.

XX

AC AAU00440;

XX

DT 18-JUN-2001 (first entry)

XX

DE Human neuropeptide receptor splice variant 2.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
 KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;
 KW cardiovascular disorder; autoimmune disorder; infectious disorder;
 KW eating behaviour disorder; narcolepsy; neurological disease;
 KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;
 KW protein co-ordinate data.

XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 47. .72
FT /label= TM1
FT /note= "Transmembrane region 1"
FT Region 83. .106
FT /label= TM2
FT /note= "Transmembrane region 2"
FT Region 112. .142
FT /label= TM3
FT /note= "Transmembrane region 3"
FT Region 163. .189
FT /label= TM4
FT /note= "Transmembrane region 4"
FT Region 214. .239
FT /label= TM5
FT /note= "Transmembrane region 5"
FT Region 299. .327
FT /label= TM6
FT /note= "Transmembrane region 6"
FT Region 335. .363
FT /label= TM7
FT /note= "Transmembrane region 7"
XX
PN WO200117532-A1.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024518.
XX
PR 10-SEP-1999; 99US-00393696.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 2001-183276/18.
DR N-PSDB; AAS00493.
XX
PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,
PT useful for preventing, treating or ameliorating obesity, narcolepsy,
PT neurological disease and addiction to narcotics, nicotine and alcohol.
XX
PS Claim 3; Fig 6; 385pp; English.
XX
CC The present sequence represents human neuropeptide receptor splice
CC variant 2. Two splice variants (AAU00439-AAU00440) and a possible mutant
CC (AAU00442) of a novel human neuropeptide receptor (AAU00438) are
CC described. The neuropeptide receptor shows sequence homology to the
CC neuropeptide Y receptor. Polypeptides and polynucleotides of the
CC neuropeptide receptor are useful for diagnosing, preventing, or treating
CC a pathological condition in a subject related to the central nervous and
CC peripheral nervous systems (CNS and PNS). The polypeptides and
CC polynucleotides may be used to treat hyperproliferative, cardiovascular,
CC autoimmune, nervous system or infectious disorders e.g. cancer, heart

CC disease, rheumatoid arthritis, Alzheimer's disease, HIV infection and
CC diabetes mellitus. In particular they are useful for preventing, treating
CC or ameliorating a medical condition in a mammal such as obesity/eating
CC behaviour disorders, narcolepsy, neurological disease, addiction to
CC narcotics, nicotine and alcohol, chronic pain, acute pain, migraine
CC headaches and anxiety disorders. The polynucleotides encoding the
CC neuropeptide receptor can also be used in gene therapy methods for
CC treating such diseases

XX

SQ Sequence 372 AA;

Query Match 100.0%; Score 1947; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-191;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEVLIAAYVAVFVA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEVLIAAYVAVFVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 241 KLWGRQIPGTTSSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSGCKEKSLVLS 372

||| ||| |||

Db 361 LSGCKEKSLVLS 372

RESULT 2

AAW06126

ID AAW06126 standard; protein; 377 AA.

XX

AC AAW06126;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor splice variant-2.

XX

KW Human; neuropeptide receptor; splice variant; drug screening;

KW receptor-agonist; receptor-antagonist; anorectic; antitumour;

KW anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;

KW sedative; diagnostic; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 46. .71
FT /note= "Transmembrane region-1"
FT Domain 82. .104
FT /note= "Transmembrane region-2"
FT Domain 110. .140
FT /note= "Transmembrane region-3"
FT Domain 160. .186
FT /note= "Transmembrane region-4"
FT Domain 210. .235
FT /note= "Transmembrane region-5"
FT Domain 293. .321
FT /note= "Transmembrane region-6"
FT Domain 329. .356
FT /note= "Transmembrane region-7".
XX
PN WO9634877-A1.
XX
PD 07-NOV-1996.
XX
PF 05-MAY-1995; 95WO-US005616.
XX
PR 05-MAY-1995; 95WO-US005616.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 1996-506094/50.
DR N-PSDB; AAT42828.
XX
PT Human neuro-peptide receptor polypeptide(s) - used to identify
PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT obesity, Alzheimer's disease, epilepsy, etc.
XX
PS Disclosure; Page 52-53; 77pp; English.
XX
CC The sequence represents human adult hypothalamus neuropeptide receptor
CC splice variant-2, which retains activity corresponding to the mature
CC receptor (AAW06124), which is structurally related to the G-protein-
CC coupled receptor family. The receptor variant contains 7 transmembrane
CC regions. The receptor may be produced in recombinant form and used in a
CC drug screening assay for isolation of receptor-agonists and -antagonists,
CC which may be used as anorectic, antitumour, anticholesterolemic,
CC neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The
CC encoding DNA may be used in genetic disease diagnosis or gene therapy.
CC The receptor itself and its corresponding antibody may also be used in
CC therapy and diagnosis
XX
SQ Sequence 377 AA;

Query Match 99.8%; Score 1944; DB 2; Length 377;
Best Local Similarity 99.7%; Pred. No. 3.2e-191;

Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
 ||||||| ||||| : ||||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 MEPSATPGAQMGVPPGSRDPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KIWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 241 KIWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSGCKEKSLVLS 372
 |||||||

Db 361 LSGCKEKSLVLS 372

RESULT 3

AAW80805

ID AAW80805 standard; protein; 389 AA.

XX

AC AAW80805;

XX

DT 29-JAN-1999 (first entry)

XX

DE Amino acid sequence of HFGAN72Y a G-protein coupled receptor.

XX

KW G-protein coupled receptor family; HFGAN72Y; mutation; probe; agonist;
 KW antagonist; activation; inhibition; gene therapy; antibody;
 KW immune response; vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia;
 KW asthma; Parkinson's disease; acute heart failure; hypotension;
 KW hypertension; urinary retention; osteoporosis; angina pectoris;
 KW myocardial infarction; ulcer; allergies; psychotic disorder;
 KW neurological disorder; gene mapping.

XX

OS Homo sapiens.

XX

PN EP875565-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308554.

XX

PR 30-APR-1997; 97US-00846705.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis C;
XX
DR WPI; 1998-570286/49.
DR N-PSDB; AAV68511.
XX
PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of HIV
PT infections, cancer, osteoporosis and Parkinson's disease.
XX
PS Claim 1; Page 7; 22pp; English.
XX
CC This is the amino acid sequence of the G-protein coupled receptor,
CC HFGAN72Y used in the method of the invention. HFGAN72Y polypeptides and
CC polynucleotides are useful for diagnosing susceptibility to diseases by
CC detecting mutations in the HFGAN72Y gene using probes containing the
CC HFGAN72Y nucleotide sequence, and can diagnose diseases associated with
CC HFGAN72Y imbalance by determining HFGAN72Y polypeptide or mRNA expression
CC levels. Agonists/antagonists can be used in treatment to activate/inhibit
CC HFGAN72Y activity, in addition to direct administration of antisense
CC sequences to prevent expression, or HFGAN72Y polypeptides to treat
CC conditions associated with a lack HFGAN72Y protein. Gene therapy may also
CC be used to affect endogenous HFGAN72Y polypeptide production. HFGAN72Y
CC antibodies are useful for inducing an immune response to immunise and
CC prevent diseases, and for isolating HFGAN72Y clones or purifying the
CC polypeptides by affinity chromatography. HFGAN72Y polypeptides can be
CC administered directly or as a vaccine to inoculate against diseases.
CC Diseases diagnosed, prevented or treated include HIV-1 or HIV-2
CC infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's
CC disease, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcers;
CC allergies, benign prostatic hypertrophy, and psychotic and neurological
CC disorders. The HFGAN72Y polypeptide is also useful for mapping the gene
CC to a chromosome, allowing gene inheritance to be studied through linkage
CC analysis
XX
SQ Sequence 389 AA;

Query Match 99.8%; Score 1943; DB 2; Length 389;
Best Local Similarity 99.7%; Pred. No. 4.3e-191;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPPASLLVDITESWLFGHALCK 120
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPPASLLVDITESWLFGHALCK 120

Qy 121 VIPYHQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 VIPYHQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGCKEKSLSVLS 372
| | | | | | |
Db 361 LSGCKEKSLSALS 372

RESULT 4

AAU11187

ID AAU11187 standard; protein; 389 AA.

XX

AC AAU11187;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72Y.

XX

KW Human; G protein-coupled receptor; GPCR; HFGAN72Y; bacterial infection;
KW fungal infection; protozoan infection; viral infection;
KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;
KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;
KW angina pectoris; renal disease; depression; schizophrenia; anorexia;
KW obesity; Kallman's syndrome; hypothalamic disorder;
KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;
KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.

XX

OS Homo sapiens.

XX

PN US2001025031-A1.

XX

PD 27-SEP-2001.

XX

PF 06-APR-2001; 2001US-00828538.

XX

PR 08-JUN-1998; 98US-0088524P.

PR 22-JUL-1998; 98US-0093726P.

PR 08-JUN-1999; 99US-00328014.

XX

PA (ELLI/) ELLIS C E.

PA (KWOK/) KWOK C.

PA (BODS/) BODSWORTH N J.

PA (HALS/) HALSEY W.

PA (HORN/) HORN S V.

XX

PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;

XX

DR WPI; 2001-624968/72.

XX

PT Isolated HFGAN72 receptor useful for treatment of a patient having need of HFGAN72 receptor and in the detection and treatment of disease, e.g. infections such as bacterial, fungal, protozoan and viral infections and cancers.

XX

PS Claim 8; Fig 3; 75pp; English.

XX

CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or its variant, encoded by the 8 exon sequences given in the specification. CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is CC administered by providing to the patient DNA encoding HFGAN72 and CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly CC useful for applications in the detection and treatment of disease, e.g. CC infections such as bacterial, fungal, protozoan and viral infections, CC particularly infections caused by human immunodeficiency virus (HIV)-1 or CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease, CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome, CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism), CC migraine, pain, lung diseases, burns, sleep disorders, jet lag, CC Huntington's disease and many other diseases and disorders given in the CC specification. The present sequence is the human HFGAN72Y receptor being CC the product of a splice variant of HFGAN72

XX

SQ Sequence 389 AA;

Query Match 99.8%; Score 1943; DB 4; Length 389;
Best Local Similarity 99.7%; Pred. No. 4.3e-191;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

QY 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAASLLVDITESWLFGHALCK 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAASLLVDITESWLFGHALCK 120

QY 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

QY 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

QY 241 KIWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 KIWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

QY 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

QY 361 LSGCKEKSLVLS 372

Db 361 LSGCKEKSLALS 372

RESULT 5

ABB08208

ID ABB08208 standard; protein; 389 AA.

XX

AC ABB08208;

XX

DT 12-MAR-2002 (first entry)

XX

DE G-protein coupled receptor (HFGAN72Y).

XX

KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer; nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy; infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer; cardiac disease; urinary retention; asthma; allergy; psychotic disorder; benign prostatic hypertrophy; neurological disorder; anxiety; delirium; schizophrenia; manic depression; dementia; mental retardation; dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2.

XX

OS Homo sapiens.

XX

PN EP1156110-A2.

XX

PD 21-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203010.

XX

PR 30-APR-1997; 97US-00846705.

PR 27-OCT-1997; 97EP-00308554.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-084320/12.

DR N-PSDB; ABA96019.

XX

PT New polynucleotide encoding a G-protein coupled receptor designated HFGAN72Y is useful to diagnose and treat associated diseases including cancer, infection, cardiac disease and psychotic and neurological disorders.

XX

PS Claim 10; Page 7; 22pp; English.

XX

CC The sequence represents G-protein coupled receptor HFGAN72Y. The invention relates to a novel isolated polynucleotide encoding HFGAN72Y polypeptide. The polypeptide of the invention has cytostatic, cardiant, analgesic, tranquillising, nootropic, neuroprotective, and anti-asthmatic activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y antagonist or competitor, or nucleic acid which inhibits HFGAN72Y expression is used to treat a subject in need of decreased HFGAN72Y activity or expression. HFGAN72Y-associated diseases include infections,

CC particularly by HIV-1 or HIV-2, cancers, anorexia, bulimia, Parkinson's
CC disease, cardiac diseases, ulcers, urinary retention, asthma, allergies,
CC benign prostatic hypertrophy, and psychotic and neurological disorders
CC including anxiety, schizophrenia, manic depression, delirium, dementia,
CC severe mental retardation and dyskinesias such as Huntington's disease
CC and Tourette's syndrome, and pain

XX

SQ Sequence 389 AA;

Query Match 99.8%; Score 1943; DB 5; Length 389;
Best Local Similarity 99.7%; Pred. No. 4.3e-191;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTATICLPPASLLVDITESWLFHALCK 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTATICLPPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSGCKEKS LVL S 372
||| ||| ||| |||
Db 361 LSGCKEKS LALS 372

RESULT 6

AAW06125

ID AAW06125 standard; protein; 369 AA.

XX

AC AAW06125;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor splice variant-1.

XX

KW Human; neuropeptide receptor; splice variant; drug screening;
receptor-agonist; receptor-antagonist; anorectic; antitumour;
anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;
sedative; diagnostic; gene therapy.

XX

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 47. .72
FT /note= "Transmembrane region-1"
FT Domain 83. .106
FT /note= "Transmembrane region-2"
FT Domain 112. .142
FT /note= "Transmembrane region-3"
FT Domain 163. .189
FT /note= "Transmembrane region-4"
FT Domain 214. .239
FT /note= "Transmembrane region-5"
FT Domain 299. .327
FT /note= "Transmembrane region-6"
FT Domain 335. .363
FT /note= "Transmembrane region-7"
XX
PN WO9634877-A1.
XX
PD 07-NOV-1996.
XX
PF 05-MAY-1995; 95WO-US005616.
XX
PR 05-MAY-1995; 95WO-US005616.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 1996-506094/50.
DR N-PSDB; AAT42827.
XX
PT Human neuro-peptide receptor polypeptide(s) - used to identify
PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT obesity, Alzheimer's disease, epilepsy, etc.
XX
PS Disclosure; Page 51-52; 77pp; English.
XX
CC The sequence represents human adult hypothalamus neuropeptide receptor
CC splice variant-1, which retains activity corresponding to the mature
CC receptor (AAW06124), which is structurally related to the G-protein-
CC coupled receptor family. The receptor variant contains 7 transmembrane
CC regions. The receptor may be produced in recombinant form and used in a
CC drug screening assay for isolation of receptor-agonists and -antagonists,
CC which may be used as anorectic, antitumour, anticholesterolemic,
CC neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The
CC encoding DNA may be used in genetic disease diagnosis or gene therapy.
CC The receptor itself and its corresponding antibody may also be used in
CC therapy and diagnosis
XX
SQ Sequence 369 AA;

Query Match 97.7%; Score 1903; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA	60
Db	1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA	60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241 KLWGRQIPGTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241 KLWGRQIPGTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361 LSG 363	
Db	361 LSG 363	

RESULT 7

AAW80456

ID AAW80456 standard; protein; 425 AA.

XX

AC AAW80456;

XX

DT 26-JAN-1999 (first entry)

XX

DE G-protein coupled receptor (HFGAN72X) polypeptide.

XX

KW G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;

KW bulimia; asthma; Parkinson's disease; acute heart failure;

KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;

KW benign prostatic hypertrophy; neurological disorder.

XX

OS Homo sapiens.

XX

PN EP875566-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308563.

XX

PR 30-APR-1997; 97US-00846704.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX
DR WPI; 1998-559432/48.
DR N-PSDB; AAV63468.
XX
PT New human G-protein coupled receptor HFGAN72X polypeptide and
PT polynucleotide - useful as diagnostic reagents and for treating e.g. HIV
PT infection, cancer and Parkinson's disease.
XX
PS Claim 1; Page 7-8; 24pp; English.
XX
CC The present sequence represents a G-protein coupled receptor (HFGAN72X)
CC polypeptide. HFGAN72X polypeptides and polynucleotides are useful for
CC diagnosing diseases related to over or under expression of HFGAN72X
CC proteins by identifying mutations in the HFGAN72X gene using HFGAN72X
CC probes, or determining HFGAN72X protein or mRNA expression levels.
CC HFGAN72X polypeptides are also useful for screening for compounds which
CC affect activity of the protein. Diseases that can be treated with
CC HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,
CC and psychotic and neurological disorders
XX
SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KIWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db 241 KIWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
Db 361 LSG 363

RESULT 8
AAU11188
ID AAU11188 standard; protein; 425 AA.
XX
AC AAU11188;
XX
DT 25-FEB-2002 · (first entry)
XX
DE Human G protein-coupled receptor HFGAN72X variant.
XX
KW Human; G protein-coupled receptor; GPCR; HFGAN72X; bacterial infection;
KW fungal infection; protozoan infection; viral infection;
KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;
KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;
KW angina pectoris; renal disease; depression; schizophrenia; anorexia;
KW obesity; Kallman's syndrome; hypothalamic disorder;
KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;
KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.
XX
OS Homo sapiens.
XX
PN US2001025031-A1.
XX
PD 27-SEP-2001.
XX
PF 06-APR-2001; 2001US-00828538.
XX
PR 08-JUN-1998; 98US-0088524P.
PR 22-JUL-1998; 98US-0093726P.
PR 08-JUN-1999; 99US-00328014.
XX
PA (ELLI/) ELLIS C E.
PA (KWOK/) KWOK C.
PA (BODS/) BODSWORTH N J.
PA (HALS/) HALSEY W.
PA (HORN/) HORN S V.
XX
PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;
XX
DR WPI; 2001-624968/72.
DR N-PSDB; AAS17464.
XX
PT Isolated HFGAN72 receptor useful for treatment of a patient having need
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.
PT infections such as bacterial, fungal, protozoan and viral infections and
PT cancers.
XX
PS Claim 23; Fig 6; 75pp; English.
XX
CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or
CC its variant, encoded by the 8 exon sequences given in the specification.
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is
CC administered by providing to the patient DNA encoding HFGAN72 and
CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
CC useful for applications in the detection and treatment of disease, e.g.

CC infections such as bacterial, fungal, protozoan and viral infections,
CC particularly infections caused by human immunodeficiency virus (HIV)-1 or
CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial
CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,
CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,
CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),
CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,
CC Huntington's disease and many other diseases and disorders given in the
CC specification. The present sequence is the human HFGAN72X variant,
CC encoded by an alternative allele of HFGAN72
XX
SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLYWRDYLKPQYEWVLIAAYVAVFVVA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLYWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAASLLVDITESWLFGHALCK 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSAVVRNWKRPSDLQGDLEQQLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 KLWGRQIPGTTSAVVRNWKRPSDLQGDLEQQLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 9

AAU11186

ID AAU11186 standard; protein; 425 AA.

XX

AC AAU11186;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72X.

XX

KW Human; G protein-coupled receptor; GPCR; HFGAN72X; bacterial infection;

KW fungal infection; protozoan infection; viral infection;
KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;
KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;
KW angina pectoris; renal disease; depression; schizophrenia; anorexia;
KW obesity; Kallman's syndrome; hypothalamic disorder;
KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;
KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.
XX

OS Homo sapiens.

XX

PN US2001025031-A1.

XX

PD 27-SEP-2001.

XX

PF 06-APR-2001; 2001US-00828538.

XX

PR 08-JUN-1998; 98US-0088524P.

PR 22-JUL-1998; 98US-0093726P.

PR 08-JUN-1999; 99US-00328014.

XX

PA (ELLI/) ELLIS C E.

PA (KWOK/) KWOK C.

PA (BODS/) BODSWORTH N J.

PA (HALS/) HALSEY W.

PA (HORN/) HORN S V.

XX

PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;

XX

DR WPI; 2001-624968/72.

XX

PT Isolated HFGAN72 receptor useful for treatment of a patient having need
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.
PT infections such as bacterial, fungal, protozoan and viral infections and
PT cancers.

XX

PS Claim 8; Fig 2; 75pp; English.

XX

CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or
CC its variant, encoded by the 8 exon sequences given in the specification.
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is
CC administered by providing to the patient DNA encoding HFGAN72 and
CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
CC useful for applications in the detection and treatment of disease, e.g.
CC infections such as bacterial, fungal, protozoan and viral infections,
CC particularly infections caused by human immunodeficiency virus (HIV)-1 or
CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial
CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,
CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,
CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),
CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,
CC Huntington's disease and many other diseases and disorders given in the
CC specification. The present sequence is the human HFGAN72X receptor being
CC the product of a splice variant of HFGAN72

XX

SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 4; Length 425;
 Best Local Similarity 100.0%; Pred. No. 6.3e-187;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120
Qy	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLKFSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLKFSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KIWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KIWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

RESULT 10

AAB67079

ID AAB67079 standard; protein; 425 AA.

XX

AC AAB67079;

XX

DT 10-APR-2001 (first entry)

XX

DE Human HFGAN72 receptor SEQ ID NO: 13.

XX

KW Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;

KW truncation mutant; ligand; neurodegenerative disorder; pain;

KW eating disorder; behaviour disorder; mood disorder?

XX

OS Homo sapiens.

XX

PN WO200100787-A2.

XX

PD 04-JAN-2001.

XX

PF 22-JUN-2000; 2000WO-US017251.

XX

PR 25-JUN-1999; 99US-0141156P.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;
XX
DR WPI; 2001-071483/08.
XX
PT Polynucleotides encoding Lig 72A polypeptides or their variants, which
PT are useful in the treatment of a disease or disorder associated with
PT pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,
PT neuropathic pain and back pain.
XX
PS Claim 8; Fig 7; 101pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC human, mouse and rat HFGAN receptor ligand Lig72A. It also provides
CC truncated mutant versions. These, and their agonists and antagonists, are
CC all useful in the treatment of eating, neurodegenerative, behaviour,
CC mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy
CC and acute inflammatory conditions
XX
SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db |||||||
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
Db |||||||
Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db |||||||
Qy 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db |||||||
Qy 241 KLGGRQIPGTTSAEVNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db |||||||
Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db |||||||
Qy 361 LSG 363
Db ||||
Qy 361 LSG 363

AAG78345

ID AAG78345 standard; protein; 425 AA.

XX

AC AAG78345;

XX

DT 22-JAN-2002 (first entry)

XX

DE Human HFGAN72X G coupled receptor polypeptide.

XX

KW Antibacterial; fungicide; virucide; protozoocide; anti-HIV; analgesic;
KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;
KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW ulcers; asthma; allergy; delirium; dementia;
KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor.

XX

OS Homo sapiens.

XX

PN EP1154019-A2.

XX

PD 14-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203008.

XX

PR 30-APR-1997; 97US-00846704.

PR 27-OCT-1997; 97EP-00308563.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-012659/02.

DR N-PSDB; AAI64172.

XX

PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
PT disease, and acute heart failure.

XX

PS Claim 11; Page 7-8; 24pp; English.

XX

CC The present sequence is that of a human HFGAN72X polypeptide encoded by a
CC cDNA shown in AAI64172. The specification describes a newly isolated
CC polynucleotide encoding a HFGAN72X G coupled receptor polypeptide. The
CC protein of the invention has antibacterial, fungicide, virucide,
CC protozoocide, anti-HIV, cardiant, analgesic, cytostatic, nootropic,
CC antiparkinsonian, antiulcer, antiasthmatic, tranquiliser, neuroleptic,
CC antidepressant, anticonvulsant and osteopathic activities. HFGAN72X
CC polynucleotides (PNs) are used to express HFGAN72X in vivo, to treat
CC diseases requiring increased activity or expression of HFGAN72X; for
CC recombinant production of HFGAN72X; diagnose diseases by detecting
CC mutations in genomic sequences and in chromosome identification and
CC mapping. HFGAN72X polypeptides are used to raise specific antibodies; as
CC therapeutic agents; to identify HFGAN72X protein-expressing clones; to
CC purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X

CC PNs are used to identify (ant)agonists of HFGAN72X, useful
CC therapeutically. Nucleic acids that inhibit expression of HFGAN72X and
CC polypeptides that compete with ligands for binding to HFGAN72X proteins
CC are also useful therapeutically and diagnostically. HFGAN72X-related
CC diseases include infections (bacterial, viral, fungal or protozoal,
CC particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;
CC manic depression; delirium; dementia; severe mental retardation and
CC dyskinesias

XX

SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 5; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLYIWRDYLKPQYEWVLIAAYVAVFVVA 60
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLYIWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFHALCK 120
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVAVTLSFIALDRWAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db 121 VIPYLQAVSVSVAVTLSFIALDRWAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPVELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db 181 AVMECSSVLPVELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KIWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db 241 KIWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
Db 361 LSG 363

RESULT 12

ABP81941

ID ABP81941 standard; protein; 425 AA.

XX

AC ABP81941;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human orexin receptor 1 protein SEQ ID NO:368.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR N-PSDB; ABZ42789.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or

CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX

SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 6; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db |||||||

1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTACILCPASLLVDITESWLFHALCK 120
Db |||||||

61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTACILCPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db |||||||

121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db |||||||

181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KIWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db |||||||

241 KIWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLVLRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db |||||||

301 MVVLLVFALCYLPISVNLVLRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363

|||

Db 361 LSG 363

RESULT 13

ABG75058

ID ABG75058 standard; protein; 425 AA.

XX

AC ABG75058;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human orexin receptor 1 protein.

XX

KW Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;
KW gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;
KW cardiant; osteopathic; antilipemic.

XX

OS Homo sapiens.

XX

PN WO2003075945-A2.

XX
PD 18-SEP-2003.
XX
PF 14-MAR-2003; 2003WO-EP002714.
XX
PR 14-MAR-2002; 2002EP-00005882.
PR 15-MAR-2002; 2002EP-00006012.
PR 20-MAR-2002; 2002EP-00006271.
PR 25-MAR-2002; 2002EP-00006810.
XX
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX
PI Eulenberg K, Steuernagel A, Haeder T, Broenner G;
XX
DR WPI; 2003-748334/70.
DR N-PSDB; ACH00818.
XX
PT New pharmaceutical composition comprising a nucleic acid molecule
PT encoding proteins regulating the energy homeostasis and metabolism of
PT triglycerides useful for detecting or preventing metabolic diseases, e.g.
PT obesity.
XX
PS Claim 3; Fig 7G; 140pp; English.
XX
CC The present invention relates to pharmaceutical compositions comprising
CC the coding sequences shown in ACH00815-ACH00827, or their encoded
CC proteins (shown in ABG75054, ABG75056-ABG75067). These are proteins
CC involved in the metabolism of triglycerides and in energy homeostasis,
CC and their coding sequences. The composition is useful for the manufacture
CC of an agent for detecting, verifying, treating, alleviating or preventing
CC disorders, including metabolic diseases such as obesity and other body-
CC weight regulation disorders as well as related disorders such as
CC metabolic syndrome, eating disorder, cachexia, diabetes mellitus,
CC hypertension, coronary heart disease, hypercholesterolaemia,
CC dyslipidaemia, osteoarthritis or gallstones, in cells, cell masses,
CC organs or subjects. The coding sequences can be used in the production of
CC transgenic animals which under- or over-produce the gene of interest. The
CC present sequence is a protein of the invention
XX
SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 7; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQEYWVLIAAYVAVFVVA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQEYWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFGHALCK 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPSDLQGDLEQQLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|||
Db 241 KLWGRQIPGTTSALVRNWKRPSDLQGDLEQQLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|||
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 14

ADK52564

ID ADK52564 standard; protein; 425 AA.

XX

AC ADK52564;

XX

DT 06-MAY-2004 (first entry)

XX

DE Hematological disorder associated Gene ID 14393 encoded protein.

XX

KW cytostatic; antianemic; antisickling; virucide; hemostatic; nephrotropic;
KW cytostatic; thrombolytic; antiparasitic; gene therapy;
KW hematologic disorder; cancer; Sickle Cell Anemia;
KW Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;
KW Retinoblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;
KW transfusion reaction; Erythroblastosis; mechanical trauma;
KW micro-angiopathic hemolytic anemia; parasite infection.

XX

OS Homo sapiens.

XX

PN WO2003065871-A2.

XX

PD 14-AUG-2003.

XX

PF 28-JAN-2003; 2003WO-US002484.

XX

PR 04-FEB-2002; 2002US-0354333P.

PR 28-FEB-2002; 2002US-0360258P.

PR 15-MAR-2002; 2002US-0364476P.

PR 26-APR-2002; 2002US-0375626P.

PR 06-JUN-2002; 2002US-0386494P.

PR 24-JUN-2002; 2002US-0390965P.

PR 28-JUN-2002; 2002US-0392480P.

PR 03-JUL-2002; 2002US-0394128P.

PR 31-JUL-2002; 2002US-0399783P.

PR 13-AUG-2002; 2002US-0403221P.

PR 30-AUG-2002; 2002US-0407045P.

PR 25-NOV-2002; 2002US-0429048P.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX
PI Carroll JM, Healy A, Weich NS, Kelly LM;
XX
DR WPI; 2003-731464/69.
DR N-PSDB; ADK52563.
XX
PT Identifying a compound capable of treating a hematologic disorder (e.g. anemia or leukemia) comprises assaying the ability of the compound to modulate the expression or activity of e.g. 131, 148, 199 or 12303 polypeptide or nucleic acid.
XX
PS Disclosure; SEQ ID NO 22; 232pp; English.
XX
CC The invention relates to a method of identifying a compound capable of treating a hematologic disorder comprises assaying the ability of the compound to modulate 131, 148, 199, 12303, 13906, 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic acid expression or polypeptide activity, thus, identifying a compound capable of treating a hematologic disorder. The methods are useful in diagnosing, preventing and treating hematological disorders, such as cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia, Polycythemia Vera, Lymphoma, Retinoblastoma, Hemophilia, disorders associated with an increased risk of Thrombosis, Herpes, Thalassemia, antibody-mediated disorders such as transfusion reactions and Erythroblastosis, mechanical trauma to red blood cells such as microangiopathic hemolytic anemias, infections by parasites or chemical injuries. The methods may also be used for identifying compounds that modulate hematological disorders. This sequence corresponds to the protein encoded by one of the genes modulated by the compounds.
XX
SQ Sequence 425 AA;

Query Match 97.78; Score 1903; DB 7; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 MEPSATPGAMGVPPGSREPSPVPPDYEDEFRLYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db |||||||
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
Db |||||||
Qy 121 VIPYHQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db |||||||
Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db |||||||
Qy 241 KLGWRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db |||||||
Qy 241 KLGWRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

QY 301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|||
Db 301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

QY 361 LSG 363
|||
Db 361 LSG 363

RESULT 15

ADL22443

ID ADL22443 standard; protein; 425 AA.

XX

AC ADL22443;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human orexin 1 receptor variant protein.

XX

KW polydipsia; single nucleotide polymorphism; SNP; orexin 1 receptor gene;
KW schizophrenia; human; mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 408

FT /note= "The wild-type residue of Ile is substituted with
FT Val at this position following a single nucleotide
FT polymorphism in the encoding gene"

XX

PN JP2004041055-A.

XX

PD 12-FEB-2004.

XX

PF 10-JUL-2002; 2002JP-00201575.

XX

PR 10-JUL-2002; 2002JP-00201575.

XX

PA (RIKA) RIKAGAKU KENKYUSHO.

XX

DR WPI; 2004-208085/20.

DR N-PSDB; ADL22427.

XX

PT Estimating whether subject has factor of polydipsia, comprises
PT determining single nucleotide polymorphism in orexin 1 receptor gene
PT and/or at least one polymorphism in linkage disequilibrium.

XX

PS Claim 11; Page; 31pp; Japanese.

XX

CC The invention relates to a novel method for estimating whether a subject
CC has a factor of polydipsia. The method comprises determining a single
CC nucleotide polymorphism (SNP) at position 1222 of a fully defined orexin
CC 1 receptor gene sequence of 1411 nucleotides, as given in the
CC specification, and/or at least one polymorphism in the linkage
CC disequilibrium from a biological sample obtained from a subject. A
CC polynucleotide of at least 10 contiguous bases comprising the SNP at

CC position 1222 is useful for estimating whether a subject comprises a
CC factor of polydipsia. A polypeptide having a polymorphic variation in the
CC human orexin 1 receptor or its fragment, or a transformed cell which
CC expresses the polypeptide is useful for the screening of a compound that
CC controls the function of the human orexin 1 receptor. The method allows
CC detection of polydipsia, which is a serious symptom of schizophrenia and
CC therefore useful in the selection of a treatment for preventing the
CC symptom. This sequence represents the variant protein following the SNP
CC at position 1222 of the 1411 nt human orexin 1 receptor gene of the
CC invention. Note: This sequence is not shown in the specification. It has
CC been created from the protein of SEQ ID No 2 and information provided in
CC claim 11 of the specification.

XX

SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 8; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPA SLLVDITESWLF GHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPA SLLVDITESWLF GHALCK 120
Qy	121 VIPYLQAVSVSVA VTL SFIALDRWYAICHPLLKSTARRARGSI LGI AVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVA VTL SFIALDRWYAICHPLLKSTARRARGSI LGI AVSLAIMVPQA 180
Qy	181 AVMECSSVLP ELANR TRLFSVC DER WADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db	181 AVMECSSVLP ELANR TRLFSVC DER WADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLWGRQIPGTT SALVRN WKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLWGRQIPGTT SALVRN WKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWL VY ANSANPIIYNF 360
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWL VY ANSANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

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Job time : 90.6501 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:43:25 ; Search time 22.6518 Seconds
(without alignments)
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Title: US-10-070-532-6

Perfect score: 1947

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1947	100.0	377	5	PCT-US95-05616-6	Sequence 6, Appli
2	1944	99.8	372	4	US-08-462-509B-6	Sequence 6, Appli
3	1943	99.8	389	2	US-08-846-705-2	Sequence 2, Appli
4	1943	99.8	389	4	US-09-211-823C-23	Sequence 23, Appli
5	1903	97.7	369	4	US-08-462-509B-4	Sequence 4, Appli
6	1903	97.7	369	5	PCT-US95-05616-4	Sequence 4, Appli
7	1903	97.7	402	4	US-08-462-509B-2	Sequence 2, Appli
8	1903	97.7	402	5	PCT-US95-05616-2	Sequence 2, Appli
9	1903	97.7	425	3	US-08-846-704-2	Sequence 2, Appli
10	1903	97.7	425	4	US-09-211-823C-22	Sequence 22, Appli
11	1897	97.4	402	3	US-08-846-704-4	Sequence 4, Appli

12	1897	97.4	425	3	US-09-479-128-2	Sequence 2, Appli
13	1341.5	68.9	444	4	US-09-426-290-2	Sequence 2, Appli
14	1340.5	68.8	444	3	US-09-119-788-2	Sequence 2, Appli
15	1307	67.1	263	3	US-08-513-974B-54	Sequence 54, Appl
16	1307	67.1	263	3	US-08-513-974B-376	Sequence 376, App
17	1307	67.1	263	4	US-09-461-436B-54	Sequence 54, Appl
18	485.5	24.9	430	3	US-09-255-368-8	Sequence 8, Appli
19	485.5	24.9	430	4	US-09-405-558-8	Sequence 8, Appli
20	480.5	24.7	432	3	US-09-255-368-2	Sequence 2, Appli
21	480.5	24.7	432	4	US-09-405-558-2	Sequence 2, Appli
22	476.5	24.5	420	3	US-09-255-368-6	Sequence 6, Appli
23	476.5	24.5	420	4	US-09-405-558-6	Sequence 6, Appli
24	472	24.2	417	4	US-09-405-558-44	Sequence 44, Appl
25	417	21.4	370	3	US-09-172-353-2	Sequence 2, Appli
26	417	21.4	370	3	US-09-172-353-3	Sequence 3, Appli
27	417	21.4	370	4	US-09-799-955-2	Sequence 2, Appli
28	417	21.4	370	4	US-09-799-955-3	Sequence 3, Appli
29	413.5	21.2	370	3	US-09-172-353-7	Sequence 7, Appli
30	413.5	21.2	370	4	US-09-799-955-7	Sequence 7, Appli
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32	413	21.2	370	3	US-08-513-974B-323	Sequence 323, App
33	413	21.2	370	3	US-09-172-353-5	Sequence 5, Appli
34	413	21.2	370	3	US-08-776-971-21	Sequence 21, Appl
35	413	21.2	370	3	US-08-776-971-104	Sequence 104, App
36	413	21.2	370	4	US-09-799-955-5	Sequence 5, Appli
37	413	21.2	370	4	US-09-461-436B-26	Sequence 26, Appl
38	413	21.2	370	4	US-09-576-290-21	Sequence 21, Appl
39	413	21.2	370	4	US-09-576-290-104	Sequence 104, App
40	406.5	20.9	370	3	US-08-776-971-140	Sequence 140, App
41	406.5	20.9	370	4	US-09-576-290-140	Sequence 140, App
42	404.5	20.8	381	2	US-08-687-355A-4	Sequence 4, Appli
43	404.5	20.8	381	4	US-09-407-367-4	Sequence 4, Appli
44	404	20.7	381	1	US-08-192-288-2	Sequence 2, Appli
45	404	20.7	381	2	US-08-687-355A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

PCT-US95-05616-6

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; Sequence 6, Application PC/TUS9505616
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
```

; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05616
; FILING DATE: concurrently
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 BASE PAIRS
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
PCT-US95-05616-6

Query Match 100.0%; Score 1947; DB 5; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.3e-178;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR	240
Db	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR	240
Qy	241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQ PRGRAFLAEVKQMRARRKTAKML	300
Db	241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQ PRGRAFLAEVKQMRARRKTAKML	300
Qy	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Qy	361 LSGCKEKSILVLS 372	
Db	361 LSGCKEKSILVLS 372	

RESULT 2
US-08-462-509B-6

; Sequence 6, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,509B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/05616
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF168P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-462-509B-6

Query Match 99.8%; Score 1944; DB 4; Length 372;
Best Local Similarity 99.7%; Pred. No. 6.3e-178;
Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
	:
Db	1 MEPSATPGAQMGVPPGSRDPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
QY	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120
QY	121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
QY	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||
Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300
|||
Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300
|||
Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
|||
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
|||
Qy 361 LSGCKEKS LVLS 372
|||
Db 361 LSGCKEKS LVLS 372

RESULT 3

US-08-846-705-2

; Sequence 2, Application US/08846705
; Patent No. 5935814
; GENERAL INFORMATION:
; APPLICANT: BERGSMA, DERK J.
; APPLICANT: ELLIS, CATHERINE E
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,705
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-705-2

Query Match 99.8%; Score 1943; DB 2; Length 389;
Best Local Similarity 99.7%; Pred. No. 8.4e-178;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVA 60
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db 121 VIPYLQAVSVSVAVLTLSFIALDRWAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGCKEKSILVLS 372
Db 361 LSGCKEKSILALS 372

RESULT 4

US-09-211-823C-23

; Sequence 23, Application US/09211823C
; Patent No. 6664229
; GENERAL INFORMATION:
; APPLICANT: HAGEN, JAMES JOSEPH
; APPLICANT: TERRETT, JONATHAN ALEXANDER
; APPLICANT: UPTON, NEIL
; APPLICANT: PIPER, DAVID
; APPLICANT: SMITH, MARTIN IAN
; APPLICANT: KENNELL, GUY ANTHONY
; APPLICANT: PATEL, SARASWATI R.
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; FILE REFERENCE: P50745
; CURRENT APPLICATION NUMBER: US/09/211,823C
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 60/069,459
; PRIOR FILING DATE: 1997-12-15

; PRIOR APPLICATION NUMBER: US 60/069,785
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 389
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-211-823C-23

Query Match 99.8%; Score 1943; DB 4; Length 389;
Best Local Similarity 99.7%; Pred. No. 8.4e-178;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60
Db |||||||
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFHALCK 120
Db |||||||
Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db |||||||
Qy 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db |||||||
Qy 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db |||||||
Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360
Db |||||||
Qy 361 LSGCKEKSILVLS 372
Db |||||||
Qy 361 LSGCKEKSILALS 372

RESULT 5

US-08-462-509B-4

; Sequence 4, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA

; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,509B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US95/05616
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wales, Michele M.
; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF168P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-509B-4

Query Match 97.7%; Score 1903; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.3e-174;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
QY	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFHALCK 120
QY	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
QY	181 AVMECSSVLPVELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR 240
Db	181 AVMECSSVLPVELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR 240
QY	241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
QY	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363

|||
Db 361 LSG 363

RESULT 6
PCT-US95-05616-4
; Sequence 4, Application PC/TUS9505616
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05616
; FILING DATE: concurrently
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 BASE PAIRS
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
PCT-US95-05616-4

Query Match 97.7%; Score 1903; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.3e-174;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
|||
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFGHALCK 120
|||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
|||
Qy 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||
Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|||
Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|||
Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
|||
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
|||
Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 7

US-08-462-509B-2

; Sequence 2, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,509B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/05616

; FILING DATE: 05-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 402 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-509B-2

Query Match 97.7%; Score 1903; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.9e-174;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
||| ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPA\$LLVDITESWLFGHALCK 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPA\$LLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTT\$ALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 KLWGRQIPGTT\$ALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 8

PCT-US95-05616-2

; Sequence 2, Application PC/TUS9505616
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05616
; FILING DATE: concurrently
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
PCT-US95-05616-2

Query Match 97.7%; Score 1903; DB 5; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.9e-174;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK	120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK	120
Qy	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241 KLWGRQIPGTTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241 KLWGRQIPGTTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Qy	361 LSG 363	
Db	361 LSG 363	

RESULT 9
US-08-846-704-2
; Sequence 2, Application US/08846704

; Patent No. 6020157
; GENERAL INFORMATION:
; APPLICANT: BERGSMA, DERK J.
; APPLICANT: ELLIS, CATHERINE E.
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,704
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-846-704-2

Query Match 97.7%; Score 1903; DB 3; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-174;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQEYEWVLIAAYVAVFVA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQEYEWVLIAAYVAVFVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAASLLVDITESWLFHALCK 120
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy	181	AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML	300
Db	241	KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML	300
Qy	301	MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSG 363	
Db	361	LSG 363	

RESULT 10

US-09-211-823C-22

; Sequence 22, Application US/09211823C
; Patent No. 6664229
; GENERAL INFORMATION:
; APPLICANT: HAGEN, JAMES JOSEPH
; APPLICANT: TERRETT, JONATHAN ALEXANDER
; APPLICANT: UPTON, NEIL
; APPLICANT: PIPER, DAVID
; APPLICANT: SMITH, MARTIN IAN
; APPLICANT: KENNEDY, GUY ANTHONY
; APPLICANT: PATEL, SARASWATI R.
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; FILE REFERENCE: P50745
; CURRENT APPLICATION NUMBER: US/09/211,823C
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 60/069,459
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: US 60/069,785
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS

US-09-211-823C-22

Query Match 97.7%; Score 1903; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-174;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

61. LUGNLUGLAVENNUHMETTENKELVILUSSALIUTTEERUUS

Db | 61 LVGNTLVCIAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPA
| SLVDITESWLFHALCK 120
QY | 121 VIPYLQAVSVSVALTLSFIALDRWAICHPLLFKSTAR
| RARGSI LGIWA VSLAIMVPQA 180
Db | 121 VIPYLQAVSVSVALTLSFIALDRWAICHPLLFKSTAR
| RARGSI LGIWA VSLAIMVPQA 180
QY | 181 AVMECSSVLPPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
| |||||
Db | 181 AVMECSSVLPPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
QY | 241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQM
| RARRKTAKML 300
| |||||
Db | 241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQM
| RARRKTAKML 300
QY | 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHLVYANSAANPIIYNF 360
| |||||
Db | 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHLVYANSAANPIIYNF 360
QY | 361 LSG 363
| |||
Db | 361 LSG 363

RESULT 11

US-08-846-704-4

; Sequence 4, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,704

; FILING DATE: 30-APR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-704-4

Query Match 97.4%; Score 1897; DB 3; Length 402;
Best Local Similarity 99.7%; Pred. No. 2.2e-173;
Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
QY	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120
QY	121 VIPYLQAVSVSVAVTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVAVTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
QY	181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR 240
Db	181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR 240
QY	241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
QY	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSANPIIYNF 360
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSANPIIYNF 360
QY	361 LSG 363
Db	361 LSG 363

RESULT 12
US-09-479-128-2
; Sequence 2, Application US/09479128
; Patent No. 6319710
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.1005-001
; CURRENT APPLICATION NUMBER: US/09/479,128
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/379,083

; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-479-128-2

Query Match 97.4%; Score 1897; DB 3; Length 425;
Best Local Similarity 99.7%; Pred. No. 2.4e-173;
Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Db |||||||
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120
Db |||||||
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120
Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db |||||||
Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db |||||||
Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db |||||||
Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db |||||||
Qy 361 LSG 363
Db ||||
Qy 361 LSG 363

RESULT 13

US-09-426-290-2

; Sequence 2, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.2001-000
; CURRENT APPLICATION NUMBER: US/09/426,290
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 444

; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-426-290-2

Query Match 68.9%; Score 1341.5; DB 4; Length 444;
Best Local Similarity 71.4%; Pred. No. 3.7e-120;
Matches 255; Conservative 35; Mismatches 46; Indels 21; Gaps 3;

Qy 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
Db 24 TQEFPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCAVWKH 83

Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL 135
Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVAL 143

Qy 136 TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPPELANR 195
Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNISIIWIVSCITIMIPQAIVMECSTVFPGLANK 203

Qy 196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSA 255
Db 204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVAYLQIFRKLWCRQIPGTSSVVQ 263

Qy 256 RNWKRPQSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
Db 264 RKWK-----PLQPVSQPRGPQOPTKSRMSAVAAEIKQIRARRKTARMLMVLLV 312

Qy 307 FALCYLPISVLNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
Db 313 FAICYLPISILNVLKRVFGMFAHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 14

US-09-119-788-2

; Sequence 2, Application US/09119788
; Patent No. 6166193
; GENERAL INFORMATION:
; APPLICANT: Yanagisawa, Masashi
; TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119,788
; FILING DATE: 21-JUL-1998

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,790
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GH50029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5515
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-119-788-2

Query Match 68.8%; Score 1340.5; DB 3; Length 444;
Best Local Similarity 71.4%; Pred. No. 4.6e-120;
Matches 255; Conservative 35; Mismatches 46; Indels 21; Gaps 3;

Qy	17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
	:: : : : : : : : :
Db	24 TQEPEFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83
Qy	76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL 135
	: : : : :
Db	84 HMRTVTNYFIVNLSLADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVAL 143
Qy	136 TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPPELANR 195
	: : : : : :
Db	144 TLSCIALDRWYAICHPLMFKSTAKRARNIVIIWIVSCIIMIPQAIVMECSTVFPGLANK 203
Qy	196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSALV 255
	: : : : : : : :
Db	204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKWLCRQIPGTSSVQ 263
Qy	256 RNWKRPQSDQLGDLEQQLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
	: : : :
Db	264 RKWK-----PLQPVSQPRGPQPTKSRMGAVAAEIKQIRARRKTARMLMVLLV 312
Qy	307 FACYLPISVLNVLRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNFLSG 363
	: : : :
Db	313 FAICYLPISILNVLRVFGMFAHTEDRETYYAWFTFSHLVYANSAANPIIYNFLSG 369

RESULT 15

US-08-513-974B-54

; Sequence 54, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji

; APPLICANT: Hosoya, Masaki

; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:

; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-513-974B-54

Query Match 67.1%; Score 1307; DB 3; Length 263;
Best Local Similarity 96.2%; Pred. No. 3.8e-117;
Matches 253; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy	91	ADVLVTAICLCPASLLVDITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIALDRWYAICH	150
Db	1	ADVLVTAICLCPASLLVDITESWLFGHALCKVIPYLQAVSVVVTLSSIALDRWYAICH	60
Qy	151	PLLFKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPLEANRTRLFSVCDERWADDL	210
Db	61	PLLFKSTARRARGSILGIWAVSLAVMVPQAAVMECSSVLPLEANRTRLLSVCDERWADDL	120
Qy	211	YPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSAVRNWKRPSDQLGDLEQ	270
Db	121	YPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSAVRNWKRPSDQLDDQGQ	180
Qy	271	GLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQA	330
Db	181	GLSSEPQPRARAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQA	240
Qy	331	SDREAVYACFTSHWLVYANSAA	353
Db	241	SDREAIYACFTSHWLVYANSAA	263

Search completed: October 14, 2004, 10:58:13
Job time : 23.6518 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:42:40 ; Search time 19.7804 Seconds
(without alignments)
1809.496 Million cell updates/sec

Title: US-10-070-532-6

Perfect score: 1947

Sequence: 1 MEPSATPGAQMGVPPGSREP.....ANPIIYNFLSGCCKEKSILVLS 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	422.5	21.7	449	2	A41738	neuropeptide Y rec
2	413.5	21.2	370	1	I52315	G protein-coupled
3	404	20.7	381	2	I39187	neuropeptide Y pep
4	391	20.1	427	2	S50150	gastric CCK-A rece
5	383.5	19.7	465	1	JQ1517	neurokinin 3 recep
6	382.5	19.6	519	2	S17783	tachykinin recepto
7	382	19.6	452	2	A34916	neurokinin 3 recep
8	379.5	19.5	452	2	JC2459	gastrin/cholecysto
9	379	19.5	584	2	JC7809	sulfakinin recepto
10	376.5	19.3	450	2	JQ1614	gastrin receptor -
11	376	19.3	385	2	S55524	neurokinin 3 recep
12	373.5	19.2	428	2	JN0692	cholecystokinin ty
13	373.5	19.2	452	2	A46195	cholecystokinin B

14	373	19.2	447	2	A47430	gastrin/cholecysto
15	371.5	19.1	423	2	B40470	glucocorticoid-ind
16	369.5	19.0	430	2	I51898	cholecystokinin A
17	368	18.9	402	2	I56595	neurokinin 2 recep
18	368	18.9	440	2	A44081	kappa-type opioid
19	367	18.8	349	2	I59336	galanin receptor 1
20	367	18.8	366	2	S71152	neuropeptide Y/pep
21	365	18.7	453	2	S32817	gastrin receptor -
22	362.5	18.6	407	2	S23510	neurokinin 1 recep
23	361	18.5	384	1	S00516	neurokinin 2 recep
24	361	18.5	444	2	A42685	cholecystokinin re
25	360	18.5	398	1	JQ1059	neurokinin 2 recep
26	359.5	18.5	407	1	JQ1274	neurokinin 1 recep
27	359.5	18.5	480	2	I53053	beta 1 adrenergic
28	359	18.4	423	2	JC7677	allatostatin recep
29	358.5	18.4	407	2	A34357	neurokinin 1 recep
30	358	18.4	477	1	QRHUB1	beta-1-adrenergic
31	357.5	18.4	407	2	S20304	neurokinin 1 recep
32	355.5	18.3	387	2	JC5949	galanin receptor 2
33	355	18.2	384	2	I57957	neurokinin 2 recep
34	354	18.2	394	2	JC7209	galanin receptor -
35	353.5	18.2	443	2	D40470	glucocorticoid-ind
36	353	18.1	390	2	A36737	neurokinin 2 recep
37	351	18.0	390	2	B41007	bombesin receptor,
38	350	18.0	483	2	A25896	beta-adrenergic re
39	348.5	17.9	436	2	JC5599	cholecystokinin-A
40	345.5	17.7	466	2	S36794	beta-1-adrenergic
41	345.5	17.7	504	2	A41783	tachykinin recepto
42	344	17.7	464	2	S12591	beta-1-adrenergic
43	343	17.6	375	2	S63685	neuropeptide Y rec
44	342	17.6	375	2	I39182	neuropeptide Y/pep
45	342	17.6	384	2	S20303	neurokinin 2 recep

ALIGNMENTS

RESULT 1

A41738

neuropeptide Y receptor - fruit fly (*Drosophila melanogaster*)

N;Alternate names: G protein-coupled receptor PR4

C;Species: *Drosophila melanogaster*

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C;Accession: A41738

R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.

J. Biol. Chem. 267, 9-12, 1992.

A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide Y receptor from *Drosophila melanogaster*.

A;Reference number: A41738; MUID:92112730; PMID:1370455

A;Accession: A41738

A;Molecule type: mRNA

A;Residues: 1-449 <LIA>

A;Cross-references: UNIPROT:P25931; GB:M81490; NID:g157996; PIDN:AAA28727.1;
PID:g157997

C;Genetics:

A;Gene: FlyBase:NepYr

A;Cross-references: FlyBase:FBgn0004842

C;Superfamily: neurokinin 1 receptor

C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 21.7%; Score 422.5; DB 2; Length 449;
Best Local Similarity 29.7%; Pred. No. 3.5e-28;
Matches 102; Conservative 61; Mismatches 128; Indels 53; Gaps 8;

Qy 26 DYEDEFRLWRDLYLPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFI 85
| : | | | :: :: | : | : || : | | : | : | : | : | : | : | : | : |
Db 75 DYD-----LLSEDMWSSAYFKIIVYMLYIPIFIFALIGNGTVCYIVYSTPRMRTVTNYFI 129

Qy 86 VNLSLADVLVTAICLPPASLL-VDITESWLFHALCKVIPYLQAVSVSVALTLSFIALDR 144
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 130 ASLAIGDILMSFFCEPSSFISLFLINYWPFGALCHFVNYSQAVSVLVSAYTLVAISIDR 189

Qy 145 WYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQAAVMECSSVLPPELANRTRLFSVCDE 204
: | | | : | | | | | : | : | : | : | : | : | : | : | : | : |
Db 190 YIAIMWPLKPRITKRYATFIIAGVWFIALATALPIPIVSGLDIPMSPWHTKCEKY-ICRE 248

Qy 205 RWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTTSALVRNWKRPSDQ 264
| | | | : | : | : | : | : | : | : | : | : | : | : |
Db 249 MWPSRSQEYYYTLSLFALQFVVPLGVLIIFTYARITIRVWAKRPPGEA-----ETNRDQ 301

Qy 265 LGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVNLNKRVF 324
: | : | | : | : | : | : | : | : | : | : | : |
Db 302 -----RMARSKRKMVKMMLTVVIVFTCCWLPFNILQLL--- 334

Qy 325 GMFRQASDREAV-----YACFTFSHWLVYANSAANPIIYNFLS 362
: | | | | | : | : | : | : | : | : | : |
Db 335 -----LNDEEFAHWDPPLPYVWFAF-HWLAMSHCCYNPIIYCYMN 372

RESULT 2

I52315

G protein-coupled receptor UHR-1 - rat

C;Species: Rattus sp. (rat)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000

C;Accession: I52315

R;Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.

Biochem. Biophys. Res. Commun. 209, 606-613, 1995

A;Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned from rat hypothalamus.

A;Reference number: I52315; MUID:95251659; PMID:7733930

A;Accession: I52315

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-370 <RES>

A;Cross-references: GB:S77867; NID:g998527; PIDN:AAB34129:1; PID:g998528

C;Superfamily: neurokinin 1 receptor

Query Match 21.2%; Score 413.5; DB 1; Length 370;
Best Local Similarity 31.6%; Pred. No. 1.7e-27;
Matches 101; Conservative 64; Mismatches 114; Indels 41; Gaps 6;

Qy 44 QYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPS 103
| : :: | | | | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 58 QLKGLIVMLYSIVVVVGLGNCLLVLVIARVRLHNVTNFLIGNLALSVDLMCAACVPLT 117

Qy	104 LLVDI-TESWLFGHALCKVIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRAR	162
	: :: : : : : : : :: :	
Db	118 LAYAFEPRGWVFGGGLCHLVFFLQPVTYVSVFTLTTIAVDRYVVLVHPLRRISLKLSA	177
Qy	163 GSILGIWAVSLAIMVPQAAVMECSSVLPLEANRTRLFSVCDERW-ADDLYPKIYHSCFFI	221
	:: : : : : : : : : :	
Db	178 YAVLGIWALSAVLALPAAVHTYHVELKP---HDVRL---CEEFWGSQERQRQIYAWGLLL	231
Qy	222 VTYLAPLGLMAMAYFQIFRKILWGRQIPGTTSLAVRNWKRPSDLQGDLEQGLSGEPQPRGR	281
	: :: : : : : :	
Db	232 GTYLLPLLAILLSYVRVSVKLRNRVVPGSVTQSQADWDR-----	270
Qy	282 AFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFT	341
	: : : : : : : : : : :	
Db	271 -----ARRRTFCLLVVVVVFALCWPLHIFNLLR---DLDPRAIDPYAFGLVQL	318
Qy	342 FSHWLVYANSAANPIIYNFL	361
	::: :	
Db	319 LCHWLAMSSACYNPFIIYAWL	338

RESULT 3

I39187

neuropeptide Y/peptide YY receptor Y2 - human

N;Alternate names: neuropeptide y/peptide YY receptor type 2

C;Species: Homo sapiens (man)

C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C;Accession: I39187; I39163; G02301

R;Gerald, C.; Walker, M.W.; Vaysse, P.J.

J. Biol. Chem. 270, 26758-26761, 1995

A;Title: Expression cloning and pharmacological characterization of a human hippocampal neuropeptide Y/peptide YY Y2 receptor subtype.

A;Reference number: I39187; MUID:96070760; PMID:7592910

A;Accession: I39187

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-381 <GER>

A;Cross-references: UNIPROT:P49146; EMBL:U36269; NID:g1063633; PIDN: AAC50281.1; PID:g1063634

R;Rose, P.M.; Fernandes, P.; Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kienzle, B.; Seethala, R.

J. Biol. Chem. 270, 22661-22664, 1995

A;Title: Cloning and functional expression of a cDNA encoding a human type 2 neuropeptide Y receptor.

A;Reference number: I39163; MUID:96032678; PMID:7559383

A;Accession: I39163

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-133, 'A', 135-381 <ROS>

A;Cross-references: EMBL:U32500; NID:g1000750; PIDN: AAA93170.1; PID:g1000751

R;Ya , H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.

submitted to the EMBL Data Library, December 1995

A;Reference number: H01019

A;Accession: G02301

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
 A;Residues: 1-171,'G',173,'R',175-201,'P',203-208,'A',210-381 <YAN>
 A;Cross-references: EMBL:U42389; NID:g1314329; PIDN:AAB07760.1; PID:g1314330
 C;Genetics:
 A;Gene: GDB:NPY2R
 A;Cross-references: GDB:4365607; OMIM:162642
 A;Map position: 4q31-4q31
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thioester bond; transmembrane protein.
 F;49-76/Domain: transmembrane #status predicted <TM1>
 F;87-113/Domain: transmembrane #status predicted <TM2>
 F;166-186/Domain: transmembrane #status predicted <TM4>
 F;221-237/Domain: transmembrane #status predicted <TM5>
 F;269-291/Domain: transmembrane #status predicted <TM6>
 F;305-328/Domain: transmembrane #status predicted <TM7>
 F;123-203/Disulfide bonds: #status predicted
 F;342/Binding site: palmitate (Cys) (covalent) #status predicted
 F;372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.7%; Score 404; DB 2; Length 381;
 Best Local Similarity 27.8%; Pred. No. 1.1e-26;
 Matches 104; Conservative 71; Mismatches 133; Indels 66; Gaps 9;

Qy	3 PSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVALV 62
	:: : : :: :: ::
Db	24 PQTTPRGEL-----VPDPEPELI----DSTKLIEVQVVLILAYCSIILLGVI 66

Qy	63 GNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCKVI 122
	: : : :: : : : :
Db	67 GNSLVIHVVIKFKSMRTVTNFIANLAVADLLVNTLC LPFTLTYTLMGEWKMPVLCILV 126

Qy	123 PYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTAR RARGSILGI-WAVSLAIMVPQAA 181
	:: : : : :: :: :
Db	127 PYAQGLAVQVSTITLT VIALDRHRCIVYHESK-ISKRISFLIIGLAWGISALLASPLAI 185

Qy	182 VMECS--SVLPELANRTRLFSVCDERWADD--LYPKIYHSCFFIVTYLAPLGLMAMAYF 236
	:: : : : : :: :
Db	186 FREYSLIEIIIPDFE---IVACTEKWPGEEKSIYGTVYSLSSLLILYVLP LGIISFSYT 240

Qy	237 QIFRKWLGRQIPGTTSA LVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKT 296
	:: . : :
Db	241 RIWSKLKNHVSPGA-----ANDHYHQRRQKT 266

Qy	297 AKMLMVVLLVFA LCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWL VYANSAA NPI 356
	: :: : : : : : :
Db	267 TKMLVCVVVVFAVSWLP---LHA FQLAVDIDSQVLDLKEYKLIFTVFHIIAMCSTFANPL 323

Qy	357 IYNFLSGCKE KSLV 370
	: :: : :
Db	324 LYGMNSNYRKAFL 337

RESULT 4

S50150

gastric CCK-A receptor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Apr-2000
C;Accession: S50150

R;Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.
Biochim. Biophys. Acta 1219, 321-327, 1994

A;Title: Cloning and expression of the rabbit gastric CCK-A receptor.

A;Reference number: S50150; MUID:95002144; PMID:7918628

A;Accession: S50150

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-427 <REU>

C;Superfamily: neurokinin 1 receptor

Query Match 20.1%; Score 391; DB 2; Length 427;
Best Local Similarity 28.8%; Pred. No. 1.6e-25;
Matches 110; Conservative 79; Mismatches 149; Indels 44; Gaps 11;

Qy 8 GAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEW---VLIAAYVAVFVVALVGN 64
| |::|| | ::|| | : | || | | | :|:::|||
Db 9 GNASGIPP-----PCELGLDNETLFCLDQP---PPSKEWQPAVQILLYSLIFLLSVLGN 59

Qy 65 TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLCPASLLVDITESWLFGHALCKVIPY 124
||| : || | |||| | ::|:|::|::: | :| :|: :: : ::|| | ||| |
Db 60 TLVITVLIRNKRMRTVTNIFLLSLAISDLMLCLFCMPFNLPNLLKDFIFGSALCKTTTY 119

Qy 125 LQAVSVSVAVTLSFIALDRWYAICHPLLFK--STARRARGSILGIWAVSLAIMVPQAAV 182
| |::|: | | |::|: | ||| || : | | | | | :| ||| |
Db 120 LMGTTSVSVSTLNLAISLERYGAICKPLQSRVWQTKSHALKVIAATWCLSFAIMTPYPIY 179

Qy 183 MECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKL 242
| ::| : | ::| | : | : | : | : | : | :| | :| | :|
Db 180 ---SNLVPFTKTNNQTANMCRFILLPSDVMQAWHTFLLLFLIPGIVMMVAYGMISLEL 236

Qy 243 W-GRQIPGTTSAVRNWK-----RPSDQLGDLEQGLSGEPQPRGRA 282
: | : : : | | :| :| :| | | | :| | :| | :| | :|
Db 237 YQGIKFDSAQQKSAKERKASTGSGRFEDNDGCYLQRSKPTRQL-ELQQ-LSGGGGGRVSR 294

Qy 283 F--LAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACF 340
: : | :: :| |||:|:| | ||:|| | : : : | :| :| .
Db 295 IHSSSSAAALMAKKRVIIRMLMIVVLFFLCWMPIFSANAARAYDTV---SAERRLSGTPI 351

Qy 341 TFSHWLTVYANSAANPIIYNFLS 362

:| | | :| | ||||| |:::

Db 352 SFILLLSYTSSCVNPIIYCFMN 373

RESULT 5

JQ1517

neurokinin 3 receptor - human

N;Alternate names: neuromedin K receptor; NK-3 receptor

C;Species: Homo sapiens (man)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: JQ1517; S20435; S21237

R;Huang, R.R.C.; Cheung, A.H.; Mazina, K.E.; Strader, C.D.; Fong, T.M.

Biochem. Biophys. Res. Commun. 184, 966-972, 1992

A;Title: cDNA sequence and heterologous expression of the human neurokinin-3 receptor.

A;Reference number: JQ1517; MUID:92246993; PMID:1374246

A;Accession: JQ1517
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-465 <HUA>
A;Cross-references: UNIPROT:P29371; GB:M89473; NID:g189223; PIDN:AAA36366.1; PID:g189224
A;Experimental source: brain
R;Buell, G.; Schulz, M.F.; Arkinstall, S.J.; Maury, K.; Missotten, M.; Adami, N.; Talabot, F.; Kawashima, E.
FEBS Lett. 299, 90-95, 1992
A;Title: Molecular characterisation, expression and localisation of human neurokinin-3 receptor.
A;Reference number: S20435; MUID:92183914; PMID:1312036
A;Accession: S20435
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2, 'I', 4-62, 'R', 64-465 <BUE>
A;Cross-references: GB:S86392; NID:g246908; PIDN:AAB21706.1; PID:g246909
R;Takahashi, K.; Tanaka, A.; Hara, M.; Nakanishi, S.
Eur. J. Biochem. 204, 1025-1033, 1992
A;Title: The primary structure and gene organization of human substance P and neuromedin K receptors.
A;Reference number: S21188; MUID:92201186; PMID:1312928
A;Accession: S21237
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-438, 'F', 440-465 <TAK>
A;Cross-references: GB:X65172; NID:g35022; PIDN:CAA46291.1; PID:g825695
C;Comment: The endogenous ligand of this receptor is neurokinin 3 (neuromedin K), one of the peptides in the mammalian tachykinin system.
C;Genetics:
A;Gene: GDB:TACR3
A;Cross-references: GDB:9599126
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane protein
F;83-111/Domain: transmembrane #status predicted <TM1>
F;122-147/Domain: transmembrane #status predicted <TM2>
F;160-181/Domain: transmembrane #status predicted <TM3>
F;202-221/Domain: transmembrane #status predicted <TM4>
F;247-272/Domain: transmembrane #status predicted <TM5>
F;300-321/Domain: transmembrane #status predicted <TM6>
F;333-355/Domain: transmembrane #status predicted <TM7>
F;23,50,73/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;158-233/Disulfide bonds: #status predicted

Query Match 19.7%; Score 383.5; DB 1; Length 465;
Best Local Similarity 27.8%; Pred. No. 7.5e-25;
Matches 103; Conservative 69; Mismatches 137; Indels 61; Gaps 11;

QY 4 SATPGAQMVGPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVG 63
|::| | :|:| | || : ::|:|| | | | || | ||:|
Db 52 SSSPSA-LGLPVASPAPSQPWNLTNQFVQPSWRIAL-----WSL--AYGVVVAVAVLG 102

QY 64 NTLVCLAVWRNHMHRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIP 123
| :| : : |||||||:|||: :| : | : : : | || | :|
Db 103 NLIVIWIILAHKRMRTVTNYFLVNLAESDASMAAFNTLVNFYALHSEWYFGANYCRFQN 162

RESULT 6

S17783

tachykinin receptor homolog DTKR - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 22-Nov-1996 #sequence revision 22-Nov-1996 #text change 09-Jul-2004

C;Accession: S17783

R;Li, X.J.; Wolfgang, W.; Wu, Y.N.; North, R.A.; Forte, M.
EMBO J. 10, 3221-3229, 1991

A;Title: Cloning, heterologous expression and developmental regulation of a Drosophila receptor for tachykinin-like peptides.

A;Reference number: S17783; MUID:92007772; PMID:1717263

A; Accession: S17783

A; Molecule type: mRNA

A; Residues: 1-519 <LIX>

A;Cross-references: UNIPROT:P30975; EMBL:X62711; NID:g8505; PIDN:CAA44595.1; PID:g8506

A: Note: the

lacking 481

Indexing for GRY
C:Genetics:

A:Gene: FlyBase:Takr99D

A;Cross-references: FlyBase:FBgn0004

Cross-references: FlyBase:FBgn0004822
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; neurotransmitter receptor; transmembrane protein

```

Query Match           19.6%; Score 382.5; DB 2; Length 519;
Best Local Similarity 27.4%; Pred. No. 1e-24;
Matches 106; Conservative 61; Mismatches 147; Indels 73; Gaps 10;

    3 PSATPGAQMVGPPGSREPS-----PVPPDYED-----EFLRYLWRDYLY 41
        |   |   |||   |   |   |   |   |   |   |   |   |   |   |   |   |   |
    45 PCRTLARSSPYPPVSFNHSQTLSTDQPAVGVDAAEDAAASMETGSFAFVVPWWRQVL- 103
    42 PKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLP 101
        |   ::   :   :   ::|||   ||   :|   |   |   |||   |||   |||   |||   :|||   ::|||   :

```

Db 104 -----WSIL--FGGMVIVATGGNLIIVWIVMTTKRMRTVTNYFIVNLSIADAMVSSLNVT 156
 Qy 102 ASLLVDITESWLFGHALCKVIPYLQAVSVSVALTLSFIALDRWYAICHPLLKSTARRA 161
 : : | || | : :: : | : : | || | : || | : : |
 Db 157 FNYYYMLSDSDWPFGFYCKLSQFIAMLSICASVFTLMAISIDRYVAIIRPLQPRMSKRCN 216
 Qy 162 RGSILGIWAVSLAIMVPQAAVMECSSV-LPELANRTRLFSVCDERWAD-----DLYPKIY 215
 || | | | | : | : | : || | | | : |
 Db 217 LAIAAVIWLSTLISCPMMIYRTEEVPVRLGSNRT---VCYPEPDGPTNHSTMESLY 272
 Qy 216 HSCFFIVTYLAPLGLMAMAYFQIFRKLGGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGE 275
 : | : | | : | : | : : | : || : |
 Db 273 NILIIILTYFLPIVSMTVTYSRVGIELWGSK-----TIGE 307
 Qy 276 PQPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQASDREA 335
 || : | : : | : | | : | : | : | : | : | : |
 Db 308 CTPR-----QVENVRSKRRVVKKMIVVVLIFAICWLPHSYFIITSCYPATEAPFIQE 361
 Qy 336 VYACFTFSHWLVYANSAANPIIYNFLS 362
 : | : | : | | : | : |
 Db 362 LYLAI---YWLMNSNSMYNPIIYCWMN 385

RESULT 7

A34916

neurokinin 3 receptor - rat

N;Alternate names: neuromedin K receptor; NK-3 receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C;Accession: A34916

R;Shigemoto, R.; Yokota, Y.; Tsuchida, K.; Nakanishi, S.
J. Biol. Chem. 265, 623-628, 1990

A;Title: Cloning and expression of a rat neuromedin K receptor cDNA.

A;Reference number: A34916; MUID:90110113; PMID:2153106

A;Accession: A34916

A;Molecule type: mRNA

A;Residues: 1-452 <SHI>

A;Cross-references: UNIPROT:P16177; GB:J05189; NID:g205670; PIDN:AAA41688.1;
PID:g205671

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 19.6%; Score 382; DB 2; Length 452;
Best Local Similarity 27.8%; Pred. No. 9.7e-25;
Matches 101; Conservative 65; Mismatches 137; Indels 60; Gaps 9;

Qy 11 MGVPPGSREPSPVPPDYEDEFRLYLRDYLIPKQYEWVLIAAYVAVFVVALVGNTLVCLA 70
 : | : | : | | : : | : | | | | | | | | : | : |
 Db 45 LGLPATTQAPSQVRANLTNQFVQPSWRIAL-----WSL--AYGLVVAVAVFGNLIVIWI 96
 Qy 71 VWRNHHMRTVTNYFIVNLSLADVLVTAICLPSALLVDITESWLFGHALCKVIPYLQAVSV 130
 : : | | | | | : | : | | : : | | | | : : | : |
 Db 97 ILAHKRMRTVTNYFLVNLAFSDASVAAFNTLINFIYGLHSEWYFGANYCRFQNFFPITAV 156
 Qy 131 SVAVLTLFSIALDRWYAICHPLLKSTARARGSILGIWAVSLAIMVPQAAVMECSSVLP 190
 : : : | | : | | : : | : | | : : | | | : | : |
 Db 157 FASIYSMTAIAVDRYMAIIDPLKPLRSATATKIVIGSIWILAFLLAFPQCLY---SKIK 212

Qy	191 ELANRTRLFSVCDERWADDLYPK---IYHSCFFIVTYLAPLGLMAMAYFQIFRKWLWGRQI	247
	: : : : : : : : : :	
Db	213 VMPGRT----LCYVQWPEG--PKQHFTYHIIIVIILVYCFPLLIMGVTYTIVGITLWGGEI	266
Qy	248 PGTT SALVRNWKRP SDQLGDLEQGLS GEPQ PRGRAFLAEVKQM RARRK TAKMLMVLLVF	307
	: : : : : : : :	
Db	267 PGDT CDKYH-----EQLKAKRKVVKMMIIVVVTF	295
Qy	308 ALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIY----NFLS	362
	: : : :: : : :: :	
Db	296 AICWL PYHVY FILTAIYQQLN RWKYI QQVYLA---SF WLAMS STMYNPII YCCLN KRFRA	352
Qy	363 GCK 365	
Db	353 GFK 355	

RESULT 8

JC2459

gastrin/cholecystokinin B receptor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C;Accession: JC2459

R;Blandizzi, C.; Song, I.; Yamada, T.

Biochem. Biophys. Res. Commun. 202, 947-953, 1994

A;Title: Molecular cloning and structural analysis of the rabbit gastrin/CCKB receptor gene.

A;Reference number: JC2459; MUID:94324990; PMID:8048969

A;Accession: JC2459

A;Molecule type: mRNA

A;Residues: 1-452 <BLA>

A;Cross-references: UNIPROT:P46627; GB:L31548; NID:g495663; PIDN:AAA31194.1; PID:g495665

C;Genetics:

A;Introns: 49/1; 133/1; 216/2; 273/1

C;Superfamily: neurokinin 1 receptor

C;Keywords: receptor; transmembrane protein

F;56-79/Domain: transmembrane #status predicted <TM1>

F;85-104/Domain: transmembrane #status predicted <TM2>

F;130-149/Domain: transmembrane #status predicted <TM3>

F;169-187/Domain: transmembrane #status predicted <TM4>

F;217-237/Domain: transmembrane #status predicted <TM5>

F;339-359/Domain: transmembrane #status predicted <TM6>

F;381-400/Domain: transmembrane #status predicted <TM7>

Query Match 19.5%; Score 379.5; DB 2; Length 452;

Best Local Similarity 27.2%; Pred. No. 1.6e-24;

Matches 100; Conservative 69; Mismatches 123; Indels 75; Gaps 9;

Qy	48 VLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVD	107
	: : : : : : : : : : : : : : : : : : : :	
Db	54 IRVTLYAVIFLMSVGGNILIIIVVLGLSRRRLRTVTNAFLSLAVSDLLLAVACMPFTLLPN	113
Qy	108 ITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFK--STARRARGSI	165
	: : : : : : : : : : : : : : : : : : : : :	
Db	114 LMGTFIFGTICKAVSYLMGVSVSTLSLVAIALERYSAICRPLQARVWQTRSAAARVI	173

Qy	166 LGIWA VSL AIMVPQA AVME C SSVL PELANRTR LFSVC DERW ADDLYPKIYHSCFFIVTYL	225
	: : : : : :: :	
Db	174 LATWLLSGLLMVPYPVYTAVQPVGPRVLQ-----CVHRWPSARVRQTWSVLLLLFF	226
Qy	226 APLGLMAMAYFQIFRK LW-----	261
	: : : :	
Db	227 VPGVVMAVAYGLISRELYLGLRFSDSDSESQR VRGQGGLP GGAAPG-----P	275
Qy	262 SDQLGDL--EQGLSGE-----PQPRGRAFL-----	294
	: : : ::	
Db	276 VHQN GRCRPEAGL AGEDGDGC YVQL PRSR PALELSALT API SGPG PGPR PAQAK -LLAKK	334
Qy	295 KTA KMLMVLLV FALCYLP I SVLN VL KRVFG MFR QAS DRE AVYACFTF SHWL VYAN SAAN	354
	: : : ::: : : : : : : :	
Db	335 RVVRM LLLVIVL FFMCWL PVY SANTW RAF DG--PGAH RALSGAP ISFI HLLSY ASAC VN	391
Qy	355 PIIYNFL 361	
	:: :	
Db	392 PLVYCFM 398	

RESULT 9

JC7809

sulfakinin receptor protein, DSK-R1 - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004

C;Accession: JC7809

R;Kubiak, T.M.; Larsen, M.J.; Burton, K.J.; Bannow, C.A.; Martin, R.A.; Zantello, M.R.; Lowery, D.E.

Biochem. Biophys. Res. Commun. 291, 313-320, 2002

A;Title: Cloning and functional expression of the first *Drosophila melanogaster* sulfakinin receptor DSK-R1.

A;Reference number: JC7809; PMID:11846406; MUID:21835488

A;Accession: JC7809

A;Molecule type: mRNA

A;Residues: 1-584 <KUB>

A;Cross-references: UNIPROT:Q7M3J6; GB:AX128640

C;Comment: This receptor, the first functionally active orphan *Drosophila* sulfakinin G-protein-coupled receptor, with seven transmembrane domains, has the possible roles in insect brain and/or gut functions.

C;Genetics:

A;Gene: dsk-r1

A;Map position: 17

F;115-139/Domain: transmembrane region #status predicted <TMR1>

F;149-167/Domain: transmembrane region #status predicted <TMR2>

F;189-207/Domain: transmembrane region #status predicted <TMR3>

F;229-250/Domain: transmembrane region #status predicted <TMR4>

F;275-300/Domain: transmembrane region #status predicted <TMR5>

F;431-454/Domain: transmembrane region #status predicted <TMR6>

F;467-491/Domain: transmembrane region #status predicted <TMR7>

Query Match 19.5%; Score 379; DB 2; Length 584;

Best Local Similarity 25.9%; Pred. No. 2.3e-24;

Matches 115; Conservative 72; Mismatches 141; Indels 116; Gaps 14;

Qy 3 PSATPGAQM GVPPGSREPSPVPPDY EDEF LRYLWRDYL YPKQYE WLIAAYVAVFVVALV 62

Db	96	PSSTP PASSS STSTG---MPV-----	W-LIPSYSMILLFAVL	127
Qy	63	GNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVI		122
Db	128	GNLLVISTLVQNRRMRTITNVFLNLAI SDMLLGVL CMPVTLVGTLRNFIFGEFLCKLF		187
Qy	123	PYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKS--TARRARGSILGIWAVSLAIMVPQA		180
Db	188	QFSQAASVA SS WTLVAISCERYYAICHPLRSRSWQTISHAYKIIIGFIWLGGILCMTPIA		247
Qy	181	AVMECSSVLP ELAN RTRL-FSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIF		239
Db	248	-----VFSQLIPTSRPGYCKCREFWPDQGYELFYNI LL D FL LVLPLLVL C VAYILIT		300
Qy	240	RKLW-----GRQI-----PGT-----TSALVRNWKRPSDL		265
Db	301	RTLYVGMAKDSGRILQQLPVSATTAGGSAPNPGTSSSN CIL VLTATAVYN-ENSNNNN		359
Qy	266	GDLEQGLSG-----EPQPRGRAFLA-----EV		287
Db	360	GNSEGSAGGGSTNMAT TL TTRPTAPT VI TTTTTVTLAKTSSPSIRVHD A ALRRSNEA		419
Qy	288	KQMRARRKTAKMLMVLLVFALCYLPISV N VLKRVFG-MFRQASDREAVYACFTFSH W L		346
Db	420	KTLESKKR V VKMLFVLVLEFFICWTPLYVINTMVMLIGPVVYEV D -YTAISFLQ L LL		475
Qy	347	VYANSAA NPII YNFLSGC E KSLV		370
Db	476	AYSSSCCN PITY CFMN A SFRRAFV		499

RESULT 10

JQ1614

gastrin receptor - multimammate rat (*Mastomys natalensis*)

C;Species: *Mastomys natalensis*

C;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text change 09-Jul-2004

C;Accession: JO1614

R; Nakata, H.; Matsui, T.; Ito, M.; Taniguchi, T.; Narabayashi, Y.; Arima, N.; Nakamura, A.; Kinoshita, Y.; Chihara, K.; Hosoda, S.; Chiba, T.
Biochem. Biophys. Res. Commun. 187, 1151-1157, 1992.

Biochem. Biophys. Res. Commun. 187, 1151-1157, 1992
A;Title: Cloning and characterization of gastrin receptor from ECL carcinoid tumor of *Mastomys natalensis*

A: Reference number: J01614; MUHP:02412002; PMTD:1522611

A: Reference number:
A: Accession: T01614

A,Accession: JQ1814
A: Molecular target: mRNA

A;Molecule type: mRNA
A;Residues: 1-450 <NNK>

A;Residues: 1-450 <NAK>
A;Cross-references: UNIPROT:P30796; GB:D12817; NID:g220646; PIDN:BAA02250.1;
RID:-220647

PID:g220647
C;Superfamily: neurokinin 1 receptor
C;Uniprot ID: P05598

C;Keywords: G protein-coupled receptor

transmembrane protein
F;59-83/Domain: transmembrane #status predicted <TM1>

F;87-109/Domain: transmembrane #status predicted <TM2>

F;132-150/Domain: transmembrane #status predicted <TM3

F;172-188/Domain: transmembrane #status predicted <TM4>

F;216-243/Domain: transmembrane #status predicted <TM5>

F;334-357/Domain: transmembrane #status predicted <TM6>
F;380-398/Domain: transmembrane #status predicted <TM7>
F;7,30,36/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.3%; Score 376.5; DB 2; Length 450;
Best Local Similarity 29.1%; Pred. No. 2.8e-24;
Matches 102; Conservative 67; Mismatches 135; Indels 47; Gaps 9;

Qy 48 VLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVD 107
Db : | | :|::: || |: : : :||||| |:::|:::|:|: |:| :|| :
56 IRITLYAVIFLMSIGNMLIIVVLGLSRRRLRTVTNAFLSLAVSDLLLAVACMPFTLLPN 115

Qy 108 ITESWLFGHALCKVIPYLQAVSVSVAVTLSFIALDRWAICHPLLK--STARRARGSI. 165
Db : ::|| :|| :|| ||||: | | ||||:| || : | | | |
116 LMGTFIGTVICKAVSYLMGVSVSSTLNVAIALERYSAICRPLQARVWQTRSHAARVI 175

Qy 166 LGIWAVSLAIMVPQAAVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYL 225
Db | | :| :|| | | : | || : | || : : : :: :
176 LATWLLSGLLMVPYPVYTVVQPVGPRVLQ-----CMHRWPSARVRQTWSVLLMLLFF 228

Qy 226 APLGLMAMAYFQIFRKLG-GRQIPG---TTSALVRNW-----KRPSDQLGDLEQ-G 271
Db | :||:|| | :|: | : | | | : || | | | | | |
229 IPGVVMAVAYGLISRELYLGLRFDGDNDSDTQSRVRNQGLPGGTAPGPVHQNGGCRHVT 288

Qy 272 LSGEPQ-----PRGRAFL-----AEVKQMRARRKTAKMLMVLLVFALC 310
Db ::|| | | : | : | ::|:::|:|:|:| | |
289 VAGEDNDGCYVQLPRSRLMTTLTTPTPGPGLASANQAKLLAKKRVVRMLLIVLLFFLC 348

Qy 311 YLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFL 361
Db :||| | | : | | :| | | ||::| |::| |:
349 WLPIYSANTWCADF---PGAHRALSGAPISFIHLLSYASACVNPLVYCFM 396

RESULT 11

S55524

neurokinin 3 receptor - mouse (fragment)

N;Alternate names: neuromedin K receptor; NK-3 receptor

C;Species: Mus musculus (house mouse)

C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S55524; I73045

R;Maroteaux, L.

submitted to the EMBL Data Library, June 1995

A;Reference number: S55524

A;Accession: S55524

A;Molecule type: mRNA

A;Residues: 1-385 <MAR>

A;Cross-references: UNIPROT:P47937; EMBL:X87823; NID:g861055; PIDN:CAA61088.1; PID:g861056

R;Cook, G.A.; Elliott, D.; Metwali, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstock, J.V.

J. Immunol. 152, 1830-1835, 1994

A;Title: Molecular evidence that granuloma T lymphocytes in murine schistosomiasis mansoni express an authentic substance P (NK-1) receptor.

A;Reference number: I56216; MUID:94165478; PMID:8120392

A;Accession: I73045

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 103-197, 'S', 199-266, 'P', 268-328 <COO>
A;Cross-references: GB:L27827; NID:g450288; PIDN:AAA17893.1; PID:g480780
C;Superfamily: neurokinin 1 receptor

Query Match 19.3%; Score 376; DB 2; Length 385;
Best Local Similarity 27.8%; Pred. No. 2.6e-24;
Matches 101; Conservative 64; Mismatches 138; Indels 60; Gaps 9;

Qy 11 MGVPPGSREPPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVALVGNTLVCLIA 70
Db 45 LGLPVTSQAPSQVRDNLTNQFVQPSWRIAL----WSL--AYGLVVAVAVFGNLIVIWI 96

Qy 71 VWRNHHMRTVTNYFIVNLSADVLVTAICLPA~~SLLVDITESWLFGHALCKV~~IPY~~LQAVSV~~ 130
Db 97 ILAHKRMRTVTNYFLVNLAFSDASVA~~FNTLVNF~~IYGVHSEWYFGANYCRFQNFFPITAV 156

Qy 131 SVAVLTLSFIALDRWYAICHPLL~~FK~~STAR~~RARGSI~~LGIWAVSLAIMVPQAAMECSSVLP 190
Db 157 FASIYSMTAIAVDRYMAIIDPLKPR~~LSAT~~ATKIVIGSIWILAFLA~~F~~PQCLY---SKIK 212

Qy 191 ELANRTRLFSVC~~D~~ERWADDLYPK---IYHSCFFIVTYLAP~~G~~LMAMAYFQIFRK~~L~~WG~~R~~QI 247
Db 213 VMPGRT---LCYVQWPEG--PKQHFTYH~~I~~I~~V~~I~~V~~CFPLLIMGV~~T~~Y~~T~~IVGITLWG~~G~~EI 266

Qy 248 PGTT~~SALVRNWKRP~~SDQLGDLEQGLSGEPQ~~PR~~GRAFLAEVKQMRARRKTAKMLMVLLVF 307
Db 267 LGDTCDKYH-----EQLKAKRKVVKMMIIIVVVT~~F~~ 295

Qy 308 ALCYLPISV~~NVL~~KRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIY---NFLS 362
Db 296 AICWL~~PYHVY~~FILTAIYQQLNRWKYIQQQVYLA--SF~~WLAMS~~STM~~YN~~PIIY~~CCLNKRF~~RA 352

Qy 363 GCK 365
Db 353 GFK 355

RESULT 12

JN0692

cholecystokinin type A receptor - human

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C;Accession: JN0692; JN0590

R;de Weerth, A.; Pisegna, J.R.; Huppi, K.; Wank, S.A.

Biochem. Biophys. Res. Commun. 194, 811-818, 1993

A;Title: Molecular cloning, functional expression and chromosomal localization of the human cholecystokinin type A receptor.

A;Reference number: JN0692; MUID:93343941; PMID:8343165

A;Accession: JN0692

A;Molecule type: mRNA

A;Residues: 1-428 <DEW>

A;Cross-references: UNIPROT:P32238; GB:L19315; NID:g306595; PIDN:AAA02819.1; PID:g306596

A;Experimental source: gallbladder

R;Ulrich, C.D.; Ferber, I.; Holicky, E.; Hadac, E.; Buell, G.; Miller, L.J.
Biochem. Biophys. Res. Commun. 193, 204-211, 1993

A;Title: Molecular cloning and functional expression of the human gallbladder cholecystokinin A receptor.
A;Reference number: JN0590; MUID:93277552; PMID:8503909
A;Accession: JN0590
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-428 <ULR>
A;Cross-references: GB:L13605; NID:g306490; PIDN:AAA35659.1; PID:g306491
A;Experimental source: gallbladder
C;Comment: This protein has diverse physiological roles in the gastrointestinal system where it mediates pancreatic growth and enzyme secretion, smooth muscle contraction of the gallbladder and stomach, and secretion from gastric mucosal cells.
C;Genetics:
A;Gene: GDB:CCKAR
A;Cross-references: GDB:141927; OMIM:118444
A;Map position: 4pter-4qter
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; phosphoprotein; transmembrane protein
F;40-67/Domain: transmembrane #status predicted <TM1>
F;78-104/Domain: transmembrane #status predicted <TM2>
F;116-137/Domain: transmembrane #status predicted <TM3>
F;158-178/Domain: transmembrane #status predicted <TM4>
F;208-234/Domain: transmembrane #status predicted <TM5>
F;314-332/Domain: transmembrane #status predicted <TM6>
F;350-369/Domain: transmembrane #status predicted <TM7>
F;10,24,190,299/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;245,249,260,290/Binding site: phosphate (Ser) (covalent) (by protein kinase C)
#status predicted
F;256/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Qy	289 QMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVY	348
	: ::: : : ::: :: : : : : .	
Db	304 NLMAKKRVRMLIVVVLFFLCWMPIFSANAWR---AYDTASAERRLSGTPISFILLSY	360
Qy	349 ANSAANPIIYNFLS	362
	: ::	
Db	361 TSSCVNPIIYCFMN	374

RESULT 13

A46195

cholecystokinin B receptor subtype - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A46195
 R;Wank, S.A.; Pisegna, J.R.; de Weerth, A.
 Proc. Natl. Acad. Sci. U.S.A. 89, 8691-8695, 1992
 A;Title: Brain and gastrointestinal cholecystokinin receptor family: structure and functional expression.
 A;Reference number: A46195; MUID:92409582; PMID:1528881
 A;Accession: A46195
 A;Status: preliminary
 A;Molecule type: nucleic acid
 A;Residues: 1-452 <WAN>
 A;Cross-references: UNIPROT:P30553; GB:M99418; NID:g203459; PIDN:AAA40925.1; PID:g203460
 A;Experimental source: brain
 A;Note: sequence extracted from NCBI backbone (NCBIN:114083, NCBIP:114084)
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.2%; Score 373.5; DB 2; Length 452;
 Best Local Similarity 27.2%; Pred. No. 5.1e-24;
 Matches 96; Conservative 73; Mismatches 135; Indels 49; Gaps 8;

Qy	48 VLIAAYVAVFVVALVGNTLVCLAVWRNHMHRTVTNYFIVNLSLADVLVTAICLPASLLVD	107
	: : :::: : : : : :: : :: : : : : :	
Db	56 IRITLYAVIFLMSVGGNVLIIVVGLSRRRLRTVTNAFLSLAVSDLLLAVACMPFTLLPN	115
Qy	108 ITESWLFGHALCKVIPYLQAVSVAVTLSFIALDRWYAICHPLLFK--STARRARGSI	165
	: :: : : : : :	
Db	116 LMGTFIGTICKVKAISYLMGVSVSVSTLNVAIALERYSAICRPLQARVWQTRSHAARVI	175
Qy	166 LGIWAWSLAIMVPQAAVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYL	225
	. : : : : : : : : : :	
Db	176 LATWLLSGLLMVPYPVYTMVQPVGPRVLQ-----CMHRWPSARVQQTWSVLLLLLLFF	228
Qy	226 APLGLMAMAYFQIFRKW-GRQIPGTTSLVRNWKRPSDQL-----GDLEQ-----	270
	:: : : : : : : :	
Db	229 IPGVVIAVAYGLISRELYLGLHFGENSETQSRARNQGGLPGGAAPGPVHQNGGCRPVT	288
Qy	271 GLSGEPQ-----PRGRAFLAEV-----KQMRARRKTAKMLMVLLVFA	308
	: : : : : : : : : :	
Db	289 SVAGEDSDGCCVQLPRSLEMTTPTPGPVGPRPNQAKLLAKRVRMLLVIVLLFF	348
Qy	309 LCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFL	361
	: : : : : : : : :	

RESULT 14

A47430

gastrin/cholecystokinin receptor B, short splice form - human
N;Alternate names: CCK-B/gastrin receptor; cholecystokinin-B/gastrin receptor
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47430; JC1352; A46645; A48262
R;Ito, M.; Matsui, T.; Taniguchi, T.; Tsukamoto, T.; Murayama, T.; Arima, N.;
Nakata, H.; Chiba, T.; Chihara, K.
J. Biol. Chem. 268, 18300-18305, 1993
A;Title: Functional characterization of a human brain cholecystokinin-B
receptor. A trophic effect of cholecystokinin and gastrin.
A;Reference number: A47430; MUID:93352657; PMID:8349705
A;Accession: A47430
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-447 <ITO>
A;Cross-references: UNIPROT:P32239; GB:D13305; NID:g436039; PIDN:BAA02564.1;
PID:g436040
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:136448)
R;Pisegna, J.R.; de Weerth, A.; Huppi, K.; Wank, S.A.
Biochem. Biophys. Res. Commun. 189, 296-303, 1992
A;Title: Molecular cloning of the human brain and gastric cholecystokinin
receptor: Structure, functional expression and chromosomal localization.
A;Reference number: JC1352; MUID:93080572; PMID:1280419
A;Accession: JC1352
A;Molecule type: mRNA
A;Residues: 1-447 <PI>
A;Cross-references: GB:L04473; NID:g179997; PIDN:AAA35660.1; PID:g179998
A;Experimental source: brain, gastric
R;Lee, Y.M.; Beinborn, M.; McBride, E.W.; Lu, M.; Kolakowski Jr., L.F.; Kopin,
A.S.
J. Biol. Chem. 268, 8164-8169, 1993
A;Title: The human brain cholecystokinin-B/gastrin receptor. Cloning and
characterization.
A;Reference number: A46645; MUID:93216795; PMID:7681836
A;Accession: A46645
A;Status: nucleic acid sequence not shown; not compared with conceptual
translation
A;Molecule type: mRNA
A;Residues: 1-447 <LEE>
A;Cross-references: GB:L08112; NID:g306488; PIDN:AAA35657.1; PID:g306489
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:129156)
R;Song, I.; Brown, D.R.; Wiltshire, R.N.; Gantz, I.; Trent, J.M.; Yamada, T.
Proc. Natl. Acad. Sci. U.S.A. 90, 9085-9089, 1993
A;Title: The human gastrin/cholecystokinin type B receptor gene: alternative
splice donor site in exon 4 generates two variant mRNAs.
A;Reference number: A48262; MUID:94022320; PMID:8415658
A;Accession: A48262
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-447 <RES>

A;Cross-references: GB:L10822; NID:g406075; PIDN:AAC37528.1; PID:g406076
C;Genetics:
A;Gene: GDB:CCKBR
A;Cross-references: GDB:136457; OMIM:118445
A;Map position: 11p15.5-11p15.4
A;Introns: 51/1; 135/1; 218/2; 271/1
C;Superfamily: neurokinin 1 receptor
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; hormone receptor; phosphoprotein; transmembrane protein
F;57-81/Domain: transmembrane #status predicted <TM1>
F;91-116/Domain: transmembrane #status predicted <TM2>
F;131-150/Domain: transmembrane #status predicted <TM3>
F;171-192/Domain: transmembrane #status predicted <TM4>
F;219-243/Domain: transmembrane #status predicted <TM5>
F;334-354/Domain: transmembrane #status predicted <TM6>
F;369-392/Domain: transmembrane #status predicted <TM7>
F;7,30,36/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;82,154,300,442/Binding site: phosphate (Ser) (covalent) #status predicted
F;127-205/Disulfide bonds: #status predicted
F;321/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 19.2%; Score 373; DB 2; Length 447;
Best Local Similarity 27.6%; Pred. No. 5.6e-24;
Matches 98; Conservative 70; Mismatches 129; Indels 58; Gaps 8;

Qy 48 VLIAAYVAVFVALVGNTLVCCLAVWRNHHMRTVTNYFIVNLSDLADVLVTAICLPPASLLVD 107
 : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 56 IIRITLYAVIFLMSVGGNMILIVVGLSRRRLRTVTNAFLLSLAVIDLAVACMPFTLPLP 115

Qy 108 ITESWLFGHALCKVIPYLQAVSVAVTLSFIALDRWYAIChPLLFK--STARRARGSI 165
 : ::|| :|| :|| ||||: ||: |||:|| :||| || : | | | |
Db 116 LMGTIFGTVICKAVSYLMGVSVSVAI ALE RYSAICRPLQARVWOTRSHAARVI 175

Qy 226 APIGLMAMAYFQIFRKWLW-----GRQIPGTT SALVRNWK-RPSDQLGDL 268
| :||:|| | ||:| | | | : :| : ||
Db 229 IPGVVMAVAYGLISRELYLGLRFDGDS DSDSQSRVRNQGGLPGAVHONGRCRP----- 281

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Qy      269 EQGLSGEPQ-----PRGRAFL-----AEVKQMRARRKTAKMLMVLLV 306
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Db      282 ETGAVGEDSDGCYVQLPRSRALELTALTAPGPGSGSRPTOAKLLAKKRVRMLLIVVVVI 341

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Qy 307 FALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLKYANSAANPIYNFL 361
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 Db 342 FFLCWLPVYSANTWRAFDG---PGAHRALSGAPISFIHLLSYASACVNPLVYCFM 393

RESULT 15

B40470

glucocorticoid-induced receptor precursor, short form RP23 - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 14-Feb-1992 #sequence revision 14-Feb-1992 #text change 09-Jul-2004

C;Accession: B40470

R; Harrigan, M.T.; Campbell, N.E.; Bourgeois, S

Mol. Endocrinol. 5, 1331-1338, 1991

A;Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potential G protein-coupled receptor.

A;Reference number: A40470; MUID:92123228; PMID:1663214

A; Accession: B40470

A; Status: preliminary

A: Molecule type: mRNA

A:Residues: 1-423 <HAB>

A:Cross-references: UNIPROT:P30731; CR:M80481; CR:M80610; NTDB:z192E16

CROSS REFERENCES: UNIFR01.
BTDN:AAA12883 1: BTD:g460318

C:Superfamily: neuropeptide_1_receptor

Query Match 19.1%; Score 371.5; DB 2; Length 423;
Best Local Similarity 27.5%; Pred. No. 7e-24;
Matches 103; Conservative 75; Mismatches 138; Indels 59; Gaps 10;

QY 5 ATPGAQMVGPPGSREPSPVPPDYEDEF-LRYL--WRDYLYPKQY-----EWVLIA 51
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P1 15 22 27 32 37 42 47 52 57 62 67 72 77 82 87 92 97 102 107 112 117 122 127 132 137 142 147 152 157 162 167 172 177 182 187 192 197 202 207 212 217 222 227 232 237 242 247 252 257 262 267 272 277 282 287 292 297 302 307 312 317 322 327 332 337 342 347 352 357 362 367 372 377 382 387 392 397 402 407 412 417 422 427 432 437 442 447 452 457 462 467 472 477 482 487 492 497 502 507 512 517 522 527 532 537 542 547 552 557 562 567 572 577 582 587 592 597 602 607 612 617 622 627 632 637 642 647 652 657 662 667 672 677 682 687 692 697 702 707 712 717 722 727 732 737 742 747 752 757 762 767 772 777 782 787 792 797 802 807 812 817 822 827 832 837 842 847 852 857 862 867 872 877 882 887 892 897 902 907 912 917 922 927 932 937 942 947 952 957 962 967 972 977 982 987 992 997 1002 1007 1012 1017 1022 1027 1032 1037 1042 1047 1052 1057 1062 1067 1072 1077 1082 1087 1092 1097 1102 1107 1112 1117 1122 1127 1132 1137 1142 1147 1152 1157 1162 1167 1172 1177 1182 1187 1192 1197 1202 1207 1212 1217 1222 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QY 52 AYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITES 111
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Qy 112 WLFGHALCKVIPYLQAVSVSVALTLSFIALDRWYATICHPLLFKSTARRARGSILGIWAV 171

Qy 172 SLAIMVPQAAVMECSSVLPLEANRTRLFSC--DERWADDLYPKIYHSCFFIVTYLAPLG 229

D_b .197 ATFFSLPHAI---CQKLFTFKYSEDIVRSLCLPDFPEPADLFWKYLDLATFILLYLLPLF 253
Q_v 230 LMAMAYFOLERKILWGRQLPCTTSALVBNWKRPSDOLCGI EOGI SGEORRGCNAELAFV 263

Db 254 IISVAYARVAKKLW-----LCNTIGDVTTEQYLA----- 282

Db' 283 -LRRKKKTTVKMLVLVVVLFALCWFPNACYVLLL---SSKAIHTNNALYFAF---HWFA 334

SYNTHÉSES TRANSANNULINÉES 302

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Search completed: October 14, 2004, 10:56:57

Job time : 20.7804 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:55:56 ; Search time 69.2316 Seconds
(without alignments)
1737.280 Million cell updates/sec

Title: US-10-070-532-6
Perfect score: 1947
Sequence: 1 MEPSATPGAQMGVPPGSREP.....ANPIIYNFLSGCKEKSLVLS 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

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19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match Length	DB	ID	Description
1	1944	99.8	372	10 US-09-393-696-6	Sequence 6, Appli
2	1944	99.8	372	13 US-10-077-874-6	Sequence 6, Appli
3	1943	99.8	389	9 US-09-828-538-20	Sequence 20, Appli
4	1943	99.8	389	10 US-09-211-823C-23	Sequence 23, Appli
5	1903	97.7	369	13 US-10-077-874-4	Sequence 4, Appli
6	1903	97.7	425	9 US-09-828-538-19	Sequence 19, Appli
7	1903	97.7	425	9 US-09-828-538-24	Sequence 24, Appli
8	1903	97.7	425	10 US-09-211-823C-22	Sequence 22, Appli
9	1903	97.7	425	14 US-10-225-567A-368	Sequence 368, App
10	1903	97.7	425	14 US-10-352-684A-22	Sequence 22, Appli
11	1898	97.5	425	10 US-09-826-509-549	Sequence 549, App
12	1897	97.4	402	13 US-10-077-874-2	Sequence 2, Appli
13	1897	97.4	425	9 US-09-961-848-2	Sequence 2, Appli
14	1886	96.9	402	10 US-09-393-696-2	Sequence 2, Appli
15	1875	96.3	369	10 US-09-393-696-4	Sequence 4, Appli
16	1783	91.6	427	9 US-09-730-931-2	Sequence 2, Appli
17	1342.5	69.0	460	14 US-10-081-810-46	Sequence 46, Appli
18	1341.5	68.9	444	10 US-09-992-331-19	Sequence 19, Appli
19	1341.5	68.9	444	14 US-10-081-810-45	Sequence 45, Appli
20	1341.5	68.9	444	14 US-10-225-567A-370	Sequence 370, App
21	1341.5	68.9	444	14 US-10-262-313-19	Sequence 19, Appli
22	1341.5	68.9	444	14 US-10-060-369-11	Sequence 11, Appli
23	1341.5	68.9	444	14 US-10-178-194-2	Sequence 2, Appli
24	1341.5	68.9	444	16 US-10-768-878-19	Sequence 19, Appli
25	1340.5	68.8	444	14 US-10-282-717-2	Sequence 2, Appli
26	1336.5	68.6	444	10 US-09-826-509-551	Sequence 551, App
27	1307	67.1	263	14 US-10-278-087A-54	Sequence 54, Appli
28	485.5	24.9	430	9 US-09-866-248A-8	Sequence 8, Appli
29	485.5	24.9	430	14 US-10-225-567A-658	Sequence 658, App
30	485.5	24.9	430	16 US-10-719-587-54	Sequence 54, Appli
31	485.5	24.9	441	14 US-10-292-798-890	Sequence 890, App
32	481.5	24.7	428	9 US-09-292-973-4	Sequence 4, Appli
33	480.5	24.7	432	9 US-09-866-248A-2	Sequence 2, Appli
34	480.5	24.7	432	16 US-10-719-587-37	Sequence 37, Appli
35	476.5	24.5	420	9 US-09-866-248A-6	Sequence 6, Appli
36	476.5	24.5	420	14 US-10-060-369-9	Sequence 9, Appli
37	476.5	24.5	522	14 US-10-081-810-53	Sequence 53, Appli
38	476.5	24.5	522	14 US-10-225-567A-512	Sequence 512, App
39	476.5	24.5	522	14 US-10-255-551-2	Sequence 2, Appli
40	476.5	24.5	522	15 US-10-072-012-360	Sequence 360, App
41	476.5	24.5	522	15 US-10-072-012-361	Sequence 361, App
42	476.5	24.5	522	15 US-10-276-774-2093	Sequence 2093, Ap
43	476.5	24.5	522	17 US-10-757-262-8	Sequence 8, Appli
44	472	24.2	417	15 US-10-072-012-358	Sequence 358, App
45	453	23.3	426	9 US-09-292-973-19	Sequence 19, Appli

ALIGNMENTS

RESULT 1
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 ; Sequence 6, Application US/09393696
 ; Publication No. US20030022277A1
 ; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-393-696-6

Query Match 99.8%; Score 1944; DB 10; Length 372;
Best Local Similarity 99.7%; Pred. No. 5.3e-177;
Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
		:	
Db	1	MEPSATPGAQMGVPPGSRDPSVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181	AVMECSSVLPANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSVLPANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTT SALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTT SALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Db	301	MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Qy	361	LSGCKEKSLVLS	372
Db	361	LSGCKEKSLVLS	372

RESULT 2

US-10-077-874-6

; Sequence 6, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/077,874
FILING DATE: 20-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,509
FILING DATE: 05-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: 43,975
REFERENCE/DOCKET NUMBER: PF168P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-077-874-6

Query Match 99.8%; Score 1944; DB 13; Length 372;
Best Local Similarity 99.7%; Pred. No. 5.3e-177;
Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFGHALCK 120
Db ~~~~~~:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Qy 121 VIPYLOQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Qy 121 VIPYLOQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db ~~~~~~:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db ~~~~~~:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
Qy 241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKOMRARRKTAKML 300

Db 241 KLGGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300
|||
QY 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|||
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|||
QY 361 LSGCKEKSLVLS 372
|||
Db 361 LSGCKEKSLVLS 372

RESULT 3

US-09-828-538-20

; Sequence 20, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
; APPLICANT: Ellis, Catherine E.
; APPLICANT: Kwok, Cheni
; APPLICANT: Bodsworth, Nicola J.
; APPLICANT: Halsey, Wendy
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications
; FILE REFERENCE: GH-50038-C1
; CURRENT APPLICATION NUMBER: US/09/828,538
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/088,624
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 60/093,726
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/328,014
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 389
; TYPE: PRT
; ORGANISM: HOMO SAPIENS

US-09-828-538-20

Query Match 99.8%; Score 1943; DB 9; Length 389;
Best Local Similarity 99.7%; Pred. No. 7e-177;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
|||
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
|||
QY 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
|||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
|||
QY 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
|||
Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy	181	AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSLVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSLVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF	360
Db	301	MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF	360
Qy	361	LSGCKEKSLVLS	372
Db	361	LSGCKEKSLALS	372

RESULT 4

US-09-211-823C-23

; Sequence 23, Application US/09211823C

; Publication No. US20030087801A1

; GENERAL INFORMATION:

; APPLICANT: HAGEN, JAMES JOSEPH

; APPLICANT: TERRETT, JONATHAN ALEXANDER

; APPLICANT: UPTON, NEIL

; APPLICANT: PIPER, DAVID
ADDRESS: 8METHU MR BIRM, LAM

; APPLICANT: SMITH, MARTIN IAN
; ATTORNEY: KENNEDY, GUY ANTHONY

; APPLICANT: RENNETT, GUY ANTHONY
; APPLICANT: RATTI, SARASWATI B.

APPENDANT: PATEL, SARASWATI R.
TITLE OF INVENTION: METHODS OF

, TITLE OF INVENTION: METHODS OF
: TITLE OF INVENTION: OF THE NEU

TITLE OF INVENTION: ANTAGONIST

FILE REFERENCE: P50745

; CURRENT APPLICATION NUMBER: US/09/211,82

; CURRENT FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER

; PRIOR FILING DATE: 1997-12-15

; PRIOR APPLICATION NUMBER: US 60,

; PRIOR FILING DATE: 1997-12-16

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSEQ for Windows

; SEQ ID NO 23
; LENGTH 662

; LENGTH: 385

; TYPE: PRT
; ORGANIZATION: U

ORGANISM:

9S-09-211-823C-23

JS-09-211-823C-23

Query Match . . . 99.8%; Score 1943; DB 10; Length 389;
 Best Local Similarity 99.7%; Pred. No. 7e-177;
 Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQEYWVLIAAYVAFVVA 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDFLRLWRDYLQPKQYEWVLIAAYVAVFVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLVDITESWLFGHALCK 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Qy 181 AVMECSSVLPPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db 181 AVMECSSVLPPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy 301 MVVLLVFALCYLPISVNLVKRVMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db 301 MVVLLVFALCYLPISVNLVKRVMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Qy 361 LSGCKEKS LVS 372
Db 361 LSGCKEKS LALS 372

RESULT 5

US-10-077-874-4

; Sequence 4, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-077-874-4

Query Match 97.7%; Score 1903; DB 13; Length 369;
Best Local Similarity 100.0%; Pred. No. 4.3e-173;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVEVVA 60
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTACILCPASLLVDITESWLFGHALCK 120
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTACILCPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
Db 361 LSG 363

RESULT 6

US-09-828-538-19

; Sequence 19, Application US/09828538

; Patent No. US20010025031A1

; GENERAL INFORMATION:

; APPLICANT: Ellis, Catherine E.

; APPLICANT: Kwok, Cheni

; APPLICANT: Bodsworth, Nicola J.

; APPLICANT: Halsey, Wendy

; APPLICANT: Van Horn, Stephanie

; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods

; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications

; FILE REFERENCE: GH-50038-C1

; CURRENT APPLICATION NUMBER: US/09/828,538

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/088,624
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 60/093,726
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/328,014
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-538-19

Query Match 97.7%; Score 1903; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR	240
Db	181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPGLMAMAYFQIFR	240
Qy	241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241 KLWGRQIPGTT SALVRNWKRP SDQLGD LEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301 MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Db	301 MVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Qy	361 LSG 363	
Db	361 LSG 363	

RESULT 7

US-09-828-538-24

; Sequence 24, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
; APPLICANT: Ellis, Catherine E.
; APPLICANT: Kwok, Cheni
; APPLICANT: Bodsworth, Nicola J.
; APPLICANT: Halsey, Wendy
; APPLICANT: Van Horn, Stephanie

; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications
; FILE REFERENCE: GH-50038-C1
; CURRENT APPLICATION NUMBER: US/09/828,538
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/088,624
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 60/093,726
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/328,014
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-538-24

Query Match 97.7%; Score 1903; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120
Qy	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db	181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

RESULT 8

US-09-211-823C-22

; Sequence 22, Application US/09211823C

; Publication No. US20030087801A1

; GENERAL INFORMATION:

; APPLICANT: HAGEN, JAMES JOSEPH
; APPLICANT: TERRETT, JONATHAN ALEXANDER
; APPLICANT: UPTON, NEIL
; APPLICANT: PIPER, DAVID
; APPLICANT: SMITH, MARTIN IAN
; APPLICANT: KENNEDY, GUY ANTHONY
; APPLICANT: PATEL, SARASWATI R.
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; FILE REFERENCE: P50745
; CURRENT APPLICATION NUMBER: US/09/211,823C
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 60/069,459
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: US 60/069,785
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-211-823C-22

Query Match 97.7%; Score 1903; DB 10; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAASLLVDITESWLFGHALCK 120
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db 181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db 241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
Db 361 LSG 363

RESULT 9

US-10-225-567A-368

; Sequence 368, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 368
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-225-567A-368

Query Match 97.7%; Score 1903; DB 14; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
QY	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
QY	121	VIPYLQAVSVSVAVTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
QY	181	AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
QY	241	KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
QY	301	MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Db	301	MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
QY	361	LSG 363	
Db	361	LSG 363	

RESULT 10

US-10-352-684A-22

; Sequence 22, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals Inc.

; APPLICANT: Carroll, Joseph M.

; APPLICANT: Healy, Aileen

; APPLICANT: Weich, Nadine S.

; APPLICANT: Kelly, Louise M.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303,
13906,

; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847,
1849,

; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES

; FILE REFERENCE: MPI02-019P1RNOMNIM

; CURRENT APPLICATION NUMBER: US/10/352,684A

; CURRENT FILING DATE: 2003-01-28

; PRIOR APPLICATION NUMBER: US 60/354,333

; PRIOR FILING DATE: 2002-02-04

; PRIOR APPLICATION NUMBER: US 60/360,258

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/364,476

; PRIOR FILING DATE: 2002-03-15

; PRIOR APPLICATION NUMBER: US 60/375,626

; PRIOR FILING DATE: 2002-04-26

; PRIOR APPLICATION NUMBER: US 60/386,494

; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US 60/390,965

; PRIOR FILING DATE: 2002-06-24

; PRIOR APPLICATION NUMBER: US 60/392,480

; PRIOR FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: US 60/394,128

; PRIOR FILING DATE: 2002-07-03

; PRIOR APPLICATION NUMBER: US 60/399,783

; PRIOR FILING DATE: 2002-07-31

; PRIOR APPLICATION NUMBER: US 60/403,221

; PRIOR FILING DATE: 2002-08-13

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 62

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 22

; LENGTH: 425

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-10-352-684A-22

Query Match 97.7%; Score 1903; DB 14; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120
 |||||||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPASLLVDITESWLFHALCK 120

 Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAIChPLLFKSTARRARGSiLGIWAVSLAIMVPQA 180
 |||||||
 Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAIChPLLFKSTARRARGSiLGIWAVSLAIMVPQA 180

 Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||||||
 Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

 Qy 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||||||
 Db 241 KLWGRQIPGTTSAVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

 Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360
 |||||||
 Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360

 Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 11

US-09-826-509-549

; Sequence 549, Application US/09826509
 ; Publication No. US20030204073A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lehmann-Bruinsma, Karin
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated
 Known G
 ; TITLE OF INVENTION: Protein-Coupled Receptors
 ; FILE REFERENCE: AREN-207
 ; CURRENT APPLICATION NUMBER: US/09/826,509
 ; CURRENT FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/195,747
 ; PRIOR FILING DATE: 2000-04-07
 ; PRIOR APPLICATION NUMBER: 09/170,496
 ; PRIOR FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 589
 ; SOFTWARE: PatentIn Version 2.1
 ; SEQ ID NO 549
 ; LENGTH: 425
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-826-509-549

Query Match 97.5%; Score 1898; DB 10; Length 425;
 Best Local Similarity 99.7%; Pred. No. 1.5e-172;
 Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Db 1 MEPSATPGAQMVGPPGSREPSPVPPDYEDEFRLYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db 121 VIPYLQAVSVSVAVLTLSFIALDRWAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLE QGLSGEPQ PRGRAFLAEVKQMRARRKTAKML 300
Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLE QGLSGEPQ PRGRAFLAEVKQMRARRKKML 300
Qy 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db 301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Qy 361 LSG 363
Db 361 LSG 363

RESULT 12

US-10-077-874-2

; Sequence 2, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975
; REFERENCE/DOCKET NUMBER: PF168P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 402 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-077-874-2

Query Match 97.4%; Score 1897; DB 13; Length 402;
Best Local Similarity 99.7%; Pred. No. 1.8e-172;
Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFHALCK	120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFHALCK	120
Qy	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML	300
Qy	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Db	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF	360
Qy	361 LSG 363	
Db	361 LSG 363	

RESULT 13
US-09-961-848-2
; Sequence 2, Application US/09961848
; Patent No. US20020146719A1
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.1005-004
; CURRENT APPLICATION NUMBER: US/09/961,848

; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/479,128
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/379,083
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-961-848-2

Query Match 97.4%; Score 1897; DB 9; Length 425;
Best Local Similarity 99.7%; Pred. No. 1.9e-172;
Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
|||
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFGHALCK 120
|||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
|||
Db 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||
Db 181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|||
Db 241 KLWGRQIPGTT SALVRNWKRPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVNLVLRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360
|||
Db 301 MVVLLVFALCYLPISVNLVLRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360

Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 14

US-09-393-696-2

; Sequence 2, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616

; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-393-696-2

Query Match 96.9%; Score 1886; DB 10; Length 402;
Best Local Similarity 99.2%; Pred. No. 2e-171;
Matches 360; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLYPKQYEWVLIPAYVAVFVVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120
Qy	121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db	181 AVMECSSVLPPELANRTRLFSVCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 NLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

RESULT 15

US-09-393-696-4
; Sequence 4, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509

; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-393-696-4

Query Match 96.3%; Score 1875; DB 10; Length 369;
Best Local Similarity 98.6%; Pred. No. 2e-170;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db 1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db 121 VIPYLQAVSVSVALTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db 181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db 241 KLWGRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
Db 361 LSG 363

Search completed: October 14, 2004, 11:16:37
Job time : 71.2316 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:41:50 ; Search time 97.6261 Seconds
(without alignments)
2192.441 Million cell updates/sec

Title: US-10-070-532-6

Perfect score: 1947

Sequence: 1 MEPSATPGAMGVPPGSREP.....ANPIIYNFLSGCCKEKSLVLS 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	1903	97.7	425	1	OX1R_HUMAN	O43613 homo sapien
2	1897	97.4	425	2	Q9HBV6	Q9hbv6 homo sapien
3	1783	91.6	416	1	OX1R_RAT	P56718 rattus norv
4	1781	91.5	416	2	Q6VNS3	Q6vns3 mus musculu
5	1781	91.5	416	2	AAR01326	Aar01326 mus muscu
6	1347.5	69.2	444	1	OX2R_CANFA	Q9tup7 canis famil
7	1343.5	69.0	443	2	Q6VLX3	Q6vlx3 mus musculu
8	1343.5	69.0	443	2	AAR01327	Aar01327 mus muscu
9	1343.5	69.0	443	2	AAR11294	Aar11294 mus muscu
10	1343.5	69.0	460	1	OX2R_MOUSE	P58308 mus musculu
11	1343.5	69.0	460	2	AAR01328	Aar01328 mus muscu
12	1343.5	69.0	460	2	AAR11293	Aar11293 mus muscu
13	1342.5	69.0	460	1	OX2R_RAT	P56719 rattus norv
14	1341.5	68.9	444	1	OX2R_HUMAN	O43614 homo sapien
15	1341.5	68.9	444	2	AAG28021	Aag28021 homo sapi

16	1285	66.0	364	2	Q8BV78	Q8bv78 mus musculu
17	1127	57.9	260	1	OX1R_MOUSE	P58307 mus musculu
18	972	49.9	199	2	Q80T45	Q80t45 mus musculu
19	659.5	33.9	166	2	Q8MJ13	Q8mj13 ovis aries
20	614	31.5	127	2	Q8SPR4	Q8spr4 ovis aries
21	533	27.4	109	2	Q8I010	Q8i010 bos taurus
22	485.5	24.9	430	1	NFF1_HUMAN	Q9gzq6 homo sapien
23	483	24.8	417	1	NFF2_MOUSE	Q924h0 mus musculu
24	480.5	24.7	432	1	NFF1_RAT	Q9ep86 rattus norv
25	479.5	24.6	405	2	Q924N0	Q924n0 mus musculu
26	476.5	24.5	522	1	NFF2_HUMAN	Q9y5x5 homo sapien
27	472	24.2	417	1	NFF2_RAT	Q9eqd2 rattus norv
28	463.5	23.8	399	2	Q75XU5	Q75xu5 gallus gall
29	463.5	23.8	399	2	BAC87782	Bac87782 gallus ga
30	453	23.3	432	2	Q924G9	Q924g9 rattus norv
31	443.5	22.8	758	2	Q7YU49	Q7yu49 drosophila
32	437	22.4	86	1	OX1R_PIG	O97661 sus scrofa
33	427.5	22.0	464	2	Q9VB87	Q9vb87 drosophila
34	427.5	22.0	464	2	AAF56655	Aaf56655 drosophil
35	422.5	21.7	449	1	NYR_DROME	P25931 drosophila
36	420.5	21.6	375	2	O57463	O57463 brachydanio
37	420	21.6	353	2	Q7PRC5	Q7prc5 anopheles g
38	417	21.4	370	2	Q6VMN6	Q6vmn6 mus musculu
39	417	21.4	370	2	AAQ84215	Aaq84215 mus muscu
40	415	21.3	382	1	NY2R_PIG	O02836 sus scrofa
41	413.5	21.2	370	1	GP10_RAT	Q64121 rattus norv
42	413	21.2	370	1	GP10_HUMAN	P49683 homo sapien
43	409	21.0	517	2	Q9VWR3	Q9vwr3 drosophila
44	407.5	20.9	542	2	Q9VRM0	Q9vrm0 drosophila
45	407.5	20.9	542	2	AAF50775	Aaf50775 drosophil

ALIGNMENTS

RESULT 1

OX1R_HUMAN

ID OX1R_HUMAN STANDARD; PRT; 425 AA.

AC 043613;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).

GN Name=HCRT1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98150861; PubMed=9491897;

RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,

RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,

RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,

RA McNulty D.E., Liu W.-S., Terrell J.A., Elshourbagy N.A., Bergsma D.J.,

RA Yanagisawa M.;

RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides

RT and G protein-coupled receptors that regulate feeding behavior.";
RL Cell 92:573-585(1998).
RN [2]
RP REVIEW.
RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
RA Hungs M., Mignot E.;
RT "Hypocretin/orexin, sleep and narcolepsy.";
RL Bioessays 23:397-408(2001).
RN [3]
RP REVIEW.
RX MEDLINE=21178476; PubMed=11283317;
RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RT "To eat or to sleep? Orexin in the regulation of feeding and
RT wakefulness.";
RL Annu. Rev. Neurosci. 24:429-458(2001).
CC -!- FUNCTION: Moderately selective excitatory receptor for orexin-A
CC and, with a lower affinity, for orexin-B neuropeptide. Seems to be
CC exclusively coupled to the G(q) subclass of heteromeric G
CC proteins, which activates the phospholipase C mediated signaling
CC cascade (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF041243; AAC39601.1; -.
DR Genew; HGNC:4848; HCRTR1.
DR MIM; 602392; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR GO; GO:0007631; P:feeding behavior; TAS.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
DR GO; GO:0007268; P:synaptic transmission; TAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000204; Orexin_receptor.
DR InterPro; IPR004059; Orexin_receptor1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR01521; OREXIN1R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 46 Extracellular (Potential).
FT TRANSMEM 47 67 1 (Potential).
FT DOMAIN 68 80 Cytoplasmic (Potential).
FT TRANSMEM 81 102 2 (Potential).
FT DOMAIN 103 119 Extracellular (Potential).
FT TRANSMEM 120 142 3 (Potential).
FT DOMAIN 143 164 Cytoplasmic (Potential).
FT TRANSMEM 165 185 4 (Potential).
FT DOMAIN 186 216 Extracellular (Potential).

FT	TRANSMEM	217	239	5 (Potential).
FT	DOMAIN	240	298	Cytoplasmic (Potential).
FT	TRANSMEM	299	321	6 (Potential).
FT	DOMAIN	322	336	Extracellular (Potential).
FT	TRANSMEM	337	360	7 (Potential).
FT	DOMAIN	361	425	Cytoplasmic (Potential).
FT	CARBOHYD	194	194	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	425 AA;	47521 MW;	1634083DE10CA092 CRC64;

Query Match 97.7%; Score 1903; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 3.2e-120;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Db	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFLRYLWRDYLKPQYEWVLIAAYVAVFVVA	60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK	120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK	120
Qy	121 VIPYLQAVSVSVALTLSFIALDRWYAIChPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121 VIPYLQAVSVSVALTLSFIALDRWYAIChPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241 KLWGRQIPGTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241 KLWGRQIPGTTSALVRNWKRPSDLQGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301 MVVLLVFALCYLPISVNLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361 LSG 363	
Db	361 LSG 363	

RESULT 2

Q9HBV6

ID Q9HBV6 PRELIMINARY; PRT; 425 AA.
 AC Q9HBV6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypocretin receptor-1 (Orexin receptor 1).
 GN Name=HCRT1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20429525; PubMed=10973318;
RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,
RA Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,
RA Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,
RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;
RT "A mutation in a case of early onset narcolepsy and a generalized
RT absence of hypocretin peptides in human narcoleptic brains.";
RL Nat. Med. 6:991-997(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21580342; PubMed=11723285;
RA Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,
RA Stefansson K., Gulcher J.R.;
RT "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";
RL Neurology 57:1896-1899(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Olafsdottir B.R., Stefansson R.H., Sigurdsson A., Hannesson H.H.,
RA Sainz J., Scammell T.E., Stefansson K., Gulcher J.R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yeager M., Welch R., Haque K., Bergen A.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled tissue;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled tissue;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF202084; AAG28020.1; -.
DR EMBL; AF202078; AAG28020.1; JOINED.
DR EMBL; AF202079; AAG28020.1; JOINED.
DR EMBL; AF202081; AAG28020.1; JOINED.

DR EMBL; AF202083; AAG28020.1; JOINED.
 DR EMBL; AF202082; AAG28020.1; JOINED.
 DR EMBL; AF202080; AAG28020.1; JOINED.
 DR EMBL; AY062030; AAL47214.1; -.
 DR EMBL; AY070269; AAL50221.1; -.
 DR EMBL; BC074796; AAH74796.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016499; F:orexin receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004059; Orexin_receptor1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01521; OREXIN1R.
 DR PRINTS; PR01064; OREXINR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 425 AA; 47535 MW; B650B37F3A2CA096 CRC64;

Query Match 97.4%; Score 1897; DB 2; Length 425;
 Best Local Similarity 99.7%; Pred. No. 8.1e-120;
 Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMVGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQMVGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPAASLLVDITESWLFGHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPAASLLVDITESWLFGHALCK 120
Qy	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Qy	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db	181 AVMECSSVLPPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy	241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db	241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300
Qy	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

OX1R_RAT

ID OX1R_RAT STANDARD; PRT; 416 AA.

AC P56718;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).

GN Name=Hcrtr1;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=98150861; PubMed=9491897;

RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,

RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,

RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,

RA McNulty D.E., Liu W.-S., Terrell J.A., Elshourbagy N.A., Bergsma D.J.,

RA Yanagisawa M.;

RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides and G protein-coupled receptors that regulate feeding behavior.";

RL Cell 92:573-585(1998).

RN [2]

RP REVIEW.

RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;

RA Hungs M., Mignot E.;

RT "Hypocretin/orexin, sleep and narcolepsy.";

RL Bioessays 23:397-408(2001).

RN [3]

RP REVIEW.

RX MEDLINE=21178476; PubMed=11283317;

RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;

RT "To eat or to sleep? Orexin in the regulation of feeding and wakefulness.";

RL Annu. Rev. Neurosci. 24:429-458(2001).

CC -!- FUNCTION: Moderately selective excitatory receptor for orexin-A and, with a lower affinity, for orexin-B neuropeptide. Seems to be exclusively coupled to the G(q) subclass of heteromeric G proteins, which activates the phospholipase C mediated signaling cascade.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Highly expressed in the brain in the prefrontal cortex, hippocampus, paraventricular thalamus, ventromedial hypothalamus, arcuate nucleus, dorsal raphe nucleus, and locus coeruleus. Not detected in the spleen, lung, liver, skeletal muscle, kidney and testis. Orexin receptor mRNA expression has also been reported in the adrenal gland, enteric nervous system, and pancreas.

CC -!- INDUCTION: By nutritional state, up-regulated by fasting.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AF041244; AAC40041.1; -.
DR RGD; 2787; Hcrtr1.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000204; Orexin_receptor.
DR InterPro; IPR004059; Orexin_receptor1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR01521; OREXIN1R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane.
FT DOMAIN 1 46 Extracellular (Potential).
FT TRANSMEM 47 67 1 (Potential).
FT DOMAIN 68 80 Cytoplasmic (Potential).
FT TRANSMEM 81 102 2 (Potential).
FT DOMAIN 103 119 Extracellular (Potential).
FT TRANSMEM 120 142 3 (Potential).
FT DOMAIN 143 164 Cytoplasmic (Potential).
FT TRANSMEM 165 185 4 (Potential).
FT DOMAIN 186 216 Extracellular (Potential).
FT TRANSMEM 217 239 5 (Potential).
FT DOMAIN 240 298 Cytoplasmic (Potential).
FT TRANSMEM 299 321 6 (Potential).
FT DOMAIN 322 336 Extracellular (Potential).
FT TRANSMEM 337 360 7 (Potential).
FT DOMAIN 361 416 Cytoplasmic (Potential).
FT CARBOHYD 194 194 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 416 AA; 46799 MW; 774DE7A22EA05D18 CRC64;

Query Match 91.6%; Score 1783; DB 1; Length 416;
Best Local Similarity 93.9%; Pred. No. 3.7e-112;
Matches 341; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

1 MEPSATPGAQMGVPPGSREPSVPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVA 60
||||| |||| | || :||||| ||||| ||||| ||||| ||||| :|||:
1 MEPSATPGAQPGVPTSSGEFPHLPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFLIA 60

61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFGHALCK 120

121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVZQA 180
||||| ||||| ||||| ||||| ||||| :||| |||||
121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLKSTARRARGSILGIWAVSLAVMVPQA 180

181 AVMECSSVLPLEANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
||||| ||||| ||||| ||||| :||| ||||| |||||
181 AVMECSSVLPLEANRTRLFSVCDERWADELYPKIYHSCFFFVTYLAPLGLMGMAKFQIFR 240

241 KLWGRQIPGTTTSALVRNWKRPSDQLGDLEQQLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
||||| ||||| ||||| :||| ||||| |||||
241 KLWGPQIPGTTTSALVRNWKRPSSEQLEAQHQGLCTEPQPRARAFLAEVKOMRARRKTAKML 300

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Qy      301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360
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Db      301 MVVLLVFALCYLPISVLNLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNF 360

Qy      361 LSG 363
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Db      361 LSG 363

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RESULT 4

Q6VNS3

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ID  Q6VNS3      PRELIMINARY;      PRT;    416 AA.
AC  Q6VNS3;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Orexin receptor type-1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/c;
RA  Chen J., Randeva H.S.;
RL  Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AY336083; AAR01326.1; -.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  InterPro; IPR000276; GPCR_Rhodopsn.
DR  InterPro; IPR000204; Orexin_receptor.
DR  InterPro; IPR004059; Orexin_receptor1.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRRHODOPSN.
DR  PRINTS; PR01521; OREXIN1R.
DR  PRINTS; PR01064; OREXINR.
DR  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR  PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW  Receptor.
SQ  SEQUENCE 416 AA; 46766 MW; A8958C594C365E00 CRC64;
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Query Match      91.5%; Score 1781; DB 2; Length 416;
Best Local Similarity 93.9%; Pred. No. 5.1e-112;
Matches 341; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFVA 60
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Db      1 MEPSATPGAQPGVPTSSGEPFHLPDYEDEFRLRYLWRDYLYPKQYEWVLIAAYVAVFLIA 60

Qy      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFHALCK 120
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |
Db      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSADVLVTAICLPPASLLVDITESWLFQALCK 120

Qy      121 VIPYLQAVSVSVAVTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
       ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :|||||
Db      121 VIPYLQAVSVSVAVTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAVMVPQA 180

Qy      181 AVMECSSVLPPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

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Db	181 AVMECSSVLPANRTRLFSVCDEHWADELYPKIHSCFFIVTYLAPLGLMGMAFQIFR 240
Qy	241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTA KML 300
Db	241 KLWGRQIPGTT SALVRNWKRP SEQLEAQHQGLCTEPQPRARAFLAEVKQMRARRKTA KML 300
Qy	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Db	301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTSHWLVYANSAANPIIYNF 360
Qy	361 LSG 363
Db	361 LSG 363

RESULT 5

AAR01326

ID AAR01326 PRELIMINARY; PRT; 416 AA.
 AC AAR01326;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Randeva H.S.;
 RT "Cloning and Characterization of the Mouse Type-1 Orexin Receptor
 (OX1R).";
 RT (OX1R).";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY336083; AAR01326.1; -.
 KW Receptor.
 SQ SEQUENCE 416 AA; 46766 MW; A8958C594C365E00 CRC64;

Query Match 91.5%; Score 1781; DB 2; Length 416;
 Best Local Similarity 93.9%; Pred. No. 5.1e-112;
 Matches 341; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy	1 MEPSATPGAQMGVPPGSREPSPVPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFVVA 60
Db	1 MEPSATPGAQPGVPTSSGEPFHLPPDYEDEFRLRYLWRDYLKPQYEWVLIAAYVAVFLIA 60
Qy	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFHALCK 120
Db	61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFQALCK 120
Qy	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
Db	121 VIPYLQAVSVSVALTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAVMVPA 180
Qy	181 AVMECSSVLPANRTRLFSVCDERWADDLYPKIHSCFFIVTYLAPLGLMAMAYFQIFR 240

Db 181 AVMECSSVLPPELANRTRLF SVCDEHWADEL YPKIYHSCFFIVTYLAPLGLMG MAYFQIFR 240
 Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRK TAKML 300
 ||||||| :||| ||| ||| ||| ||| ||| ||| |||
 Db 241 KLWGRQIPGTT SALVRNWKRP SEQLEAQHQGLCTEPQPRARAFLAEVKQMRARRK TAKML 300
 ||||||| ||| ||| ||| ||| ||| ||| |||
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTF SHWL VYANSAANPIIYNF 360
 ||||||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTF SHWL VYANSAANPIIYNF 360
 Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 6

OX2R_CANFA

ID OX2R_CANFA STANDARD; PRT; 444 AA.
 AC Q9TUP7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
 GN Name=HCRT R2;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99385793; PubMed=10458611;
 RA Lin L., Faraco J., Li R., Kadotani H., Rogers W., Lin X., Qiu X.,
 RA de Jong P.J., Nishino S., Mignot E.;
 RT "The sleep disorder canine narcolepsy is caused by a mutation in the
 RT hypocretin receptor 2 gene.";
 RL Cell 98:365-376(1999).
 RN [2]
 RP REVIEW.
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
 RA Hungs M., Mignot E.;
 RT "Hypocretin/orexin, sleep and narcolepsy.";
 RL Bioessays 23:397-408(2001).
 RN [3]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 RN [4]
 RP VARIANT NARCOLEPSY LYS-54, AND MUTAGENESIS OF GLU-54.
 RX MEDLINE=21180003; PubMed=11282968; DOI=10.1101/gr.161001;
 RA Hungs M., Fan J., Lin L., Lin X., Maki R.A., Mignot E.;
 RT "Identification and functional analysis of mutations in the hypocretin
 RT (orexin) genes of narcoleptic canines.";
 RL Genome Res. 11:531-539(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A

CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DISEASE: Defects in HCRTR2 are a cause of an autosomal recessive
 CC form of narcolepsy, observed in labradors, dobermans and
 CC dachshunds. Narcolepsy is a neurological sleep disorder affecting
 CC animals and humans, characterized by excessive daytime sleepiness,
 CC sleep fragmentation, symptoms of abnormal rapid-eye-movement
 CC (REM) sleep, such as cataplexy, hypnagogic hallucinations, and
 CC sleep paralysis. Cataplexy is a sudden loss of muscle tone
 CC triggered by emotions, which is the most valuable clinical feature
 CC used to diagnose narcolepsy. As in humans, most cases of canine
 CC narcolepsy are sporadic but an autosomal recessive form was also
 CC observed.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF164626; AAD49333.1; -.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Disease mutation; G-protein coupled receptor; Glycoprotein;
 KW Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 444 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).
 FT VARIANT 54 54 E -> K (in autosomal recessive
 narcolepsy).
 FT MUTAGEN 54 54 E->K: Loss of function.
 SQ SEQUENCE 444 AA; 50675 MW; D848A4536D485D6B CRC64;

Query Match 69.2%; Score 1347.5; DB 1; Length 444;
Best Local Similarity 72.9%; Pred. No. 8.1e-83;
Matches 255; Conservative 40; Mismatches 48; Indels 7; Gaps 3;

Qy 17 SREPSPVPPDYED-EFLRYLWRDYLKPQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
::|| | ||:| |||||||:||:||:||||| |: ||||||| |||:|||:||
Db 24 TQEFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALVGNVLVCVAVWKNH 83

Qy 76 HMRTVTNYFIVNLSSLADVLVTACICLPASLLVDITESWLFHALCKVIPYLQAVSVSVAVL 135
|||||:|||||:|||||:|||:|||:|||||:|||:|||:|||:|||:
Db 84 HMRTVTNYFIVNLSSLADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVL 143

Qy 136 TLSFIALDRWYAICHPLLFKSTARARGSIILGIWAVSLAIMVPQAAMECSSVLPPELANR 195
||| |||||||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNISIIWIVSCIIMIPQAIVMECSTMLPGLANK 203

Qy 196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSALV 255
| ||:||||| :|||:|||:|||:|||:|||:|||:|||:|||:
Db 204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKWLCRQIPGTSSVQ 263

Qy 256 RNWK--RPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLP 313
| || :| :| :| :| :| :| :| :| :| :| :| :| :| :|:
Db 264 RKKWPLQPASQ---PRPGQQTKSRISAAEIKQIRARRKTARMLMVLLVFAICYLP 319

Qy 314 ISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
||:|||||:|||:|||:|||:|||:|||:|||:|||:|||:
Db 320 ISIINVLKRVFGMFTHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 7

Q6VLX3

ID Q6VLX3 PRELIMINARY; PRT; 443 AA.
AC Q6VLX3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Orexin receptor type-2a.
GN Name=MOXR2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Chen J., Randeva H.S.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY339389; AAR11294.1; -.
DR EMBL; AY339383; AAR11294.1; JOINED.
DR EMBL; AY339384; AAR11294.1; JOINED.
DR EMBL; AY339385; AAR11294.1; JOINED.
DR EMBL; AY339386; AAR11294.1; JOINED.
DR EMBL; AY339387; AAR11294.1; JOINED.
DR EMBL; AY339388; AAR11294.1; JOINED.

DR EMBL; AY336084; AAR01327.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PRINTS; PR01064; OREXINR.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 69.0%; Score 1343.5; DB 2; Length 443;
 Best Local Similarity 71.7%; Pred. No. 1.5e-82;
 Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

Qy	17 SREPSPVPPDYED-EFLRYLWRDYLKPQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH	75
	:: : : : : : : : : :	
Db	24 TQEPPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAWWKNH	83
Qy	76 HMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFGHALCKVIPYLOQAVSVSVAL	135
	: : : : :	
Db	84 HMRTVTNYFIVNLSLADVLVTITCLPATLVDITETWFFGQSLCKVIPYLOQTVSVSVSL	143
Qy	136 TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPLEANR	195
	: : : : : :	
Db	144 TLSCIALDRWYAICHPLMFKSTAKRARNSTVVIWIVSCIIMIPQAAVMECSSMLPGLANK	203
Qy	196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSALV	255
	: : : : : : : :	
Db	204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPCLMILAYLQIFRKWLRCRQIPGTSSVVQ	263
Qy	256 RNWKRPQSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV	306
	: : : : : : : : : :	
Db	264 RKWKQ-----QQPVS---QPRGSGQQSKARISSAVAAEIKQIRARRKTARMLMVLLV	312
Qy	307 FACYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG	363
	: : :	
Db	313 FAICYLPISILNVLKRVFGMFTHTEDRETYYAWFTFSHWLVYANSAANPIIYNFLSG	369

RESULT 8

AAR01327

ID AAR01327 PRELIMINARY; PRT; 443 AA.
 AC AAR01327;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-2a.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Randeva H.S.;
 RT "Cloning and Characterization of the Mouse Type-2a Orexin Receptor
 RT Subtype (OX2aR).";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY336084; AAR01327.1; -.
 KW Receptor.
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 69.0%; Score 1343.5; DB 2; Length 443;
 Best Local Similarity 71.7%; Pred. No. 1.5e-82;
 Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

Qy	17 SREPSPVPPDYED-EFLRYLWRDYLKPQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75 :: : : : : : : : : :
Db	24 TQEPEFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAWKNH 83
Qy	76 HMRTVTNYFIVNLSIADVLVTAICLPPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL 135 : : : : :
Db	84 HMRTVTNYFIVNLSIADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVAL 143
Qy	136 TLSFIALDRWYAICHPLFKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPPELANR 195 : : : : :
Db	144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIWIVSCIIMIPQAIVMECSSMLPGLANK 203
Qy	196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSAEV 255 : : : : : : : :
Db	204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKWLCRQIPGTSSVQ 263
Qy	256 RNWKRPQSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306 : : : : : :
Db	264 RKWKQ-----QQPVS---QPRGSGQQSKARISSAVAEIKQIRARRKTARMLMVLLV 312
Qy	307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363 : : : :
Db	313 FAICYLPISILNVLKRVFGMFTHTEDRETYYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 9
 AAR11294

ID AAR11294 PRELIMINARY; PRT; 443 AA.
 AC AAR11294;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-2a.
 GN MOXR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;

RA Chen J., Randeva H.S.;
 RT "Genomic structure analysis of the *Mus musculus* orexin type-2 (MOXR2) gene.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY339383; AAR11294.1; JOINED.
 DR EMBL; AY339384; AAR11294.1; JOINED.
 DR EMBL; AY339385; AAR11294.1; JOINED.
 DR EMBL; AY339386; AAR11294.1; JOINED.
 DR EMBL; AY339387; AAR11294.1; JOINED.
 DR EMBL; AY339388; AAR11294.1; JOINED.
 DR EMBL; AY339389; AAR11294.1; -.
 KW Receptor.
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 69.0%; Score 1343.5; DB 2; Length 443;
 Best Local Similarity 71.7%; Pred. No. 1.5e-82;
 Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

Qy	17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH	75
	:: : : : : : :	
Db	24 TQEPEFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH	83
Qy	76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL	135
	: : : : :	
Db	84 HMRTVTNYFIVNLSLADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVAL	143
Qy	136 TLSFIALDRWYAICHPLFKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPANELNR	195
	: : : : :	
Db	144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIWIVSCIIMIPQAIVMECSSMLPGLANK	203
Qy	196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSLV	255
	: :: : : : : : :	
Db	204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQ	263
Qy	256 RNWKRPQSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV	306
	: : : : : :	
Db	264 RKWKQ-----QQPVS---QPRGSGQQSKARI SAVAEEIKQIRARRKTARMLMVLLV	312
Qy	307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHLVYANSAANPIIYNFLSG	363
	: :	
Db	313 FAICYLPISILNVLKRVFGMFTHTEDRETYYAWFTFSHLVYANSAANPIIYNFLSG	369

RESULT 10

OX2R_MOUSE

ID OX2R_MOUSE STANDARD; PRT; 460 AA.
 AC P58308; Q8BG12;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
 GN Name=Hcrtr2; Synonyms=Mox2r;
 OS *Mus musculus* (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Mus*.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).

RN [2]

RP SEQUENCE OF 100-311 FROM N.A.

RC STRAIN=C57BL/6;

RA Szendro P.I., Maevers K., Eichele G.;

RT "Cloning of mouse orexin receptors.";

RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP REVIEW.

RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;

RA Hungs M., Mignot E.;

RT "Hypocretin/orexin, sleep and narcolepsy.";

RL Bioessays 23:397-408(2001).

RN [4]

RP REVIEW.

RX MEDLINE=21178476; PubMed=11283317;

RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;

RT "To eat or to sleep? Orexin in the regulation of feeding and
RT wakefulness.";

RL Annu. Rev. Neurosci. 24:429-458(2001).

CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
CC and orexin-B neuropeptides.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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CC -----
DR EMBL; AK038551; BAC30039.1; -.
DR EMBL; AK048781; BAC33457.1; -.
DR EMBL; AF394597; AAK71327.1; -.
DR MGD; MGI:1889024; Mox2r.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR000204; Orexin_receptor.
DR InterPro; IPR004060; Orexin_receptor2.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF03827; Orexin_rec2; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR01522; OREXIN2R.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 54 Extracellular (Potential).
FT TRANSMEM 55 75 1 (Potential).
FT DOMAIN 76 88 Cytoplasmic (Potential).
FT TRANSMEM 89 110 2 (Potential).
FT DOMAIN 111 127 Extracellular (Potential).
FT TRANSMEM 128 150 3 (Potential).
FT DOMAIN 151 172 Cytoplasmic (Potential).
FT TRANSMEM 173 193 4 (Potential).
FT DOMAIN 194 224 Extracellular (Potential).
FT TRANSMEM 225 247 5 (Potential).
FT DOMAIN 248 304 Cytoplasmic (Potential).
FT TRANSMEM 305 327 6 (Potential).
FT DOMAIN 328 342 Extracellular (Potential).
FT TRANSMEM 343 366 7 (Potential).
FT DOMAIN 367 460 Cytoplasmic (Potential).
FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).
FT CONFLICT 201 201 A -> T (in Ref. 2).
FT CONFLICT 240 240 I -> V (in Ref. 2).
SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

Query Match 69.0%; Score 1343.5; DB 1; Length 460;
Best Local Similarity 71.7%; Pred. No. 1.6e-82;
Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

QY 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
::|| | |||:| |||||||:||:||:||||| | : ||||||:|| | ||:|||:|||
Db 24 TQEPLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83
QY 76 HMRTVTNYFIVNLSLADVLVTAICLPPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL 135
||||||| ||||| ||||| ||||| ||||:|:|||:| || :||||||| |||||:|||
Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVAL 143
QY 136 TLSFIALDRWYAICHPLLKSTARRARGSIILGIWAVSLAIMVPQAAMECSSVLPANR 195
||| ||||||| |||||:|||:||| ||:||| |||:||| |||||||:||| |||:

Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNSTIVVIWIVSCIIMIPQAIVMECSSMLPGLANK 203
 Qy 196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSLV 255
 | ||:|||| | ::|||:|| |||:|||:||| || :|| ||||||| |||||:| :
 Db 204 TTLFTVCDEHWGGEVYPKMYHICFLVTYMAPLCLMILAYLQIFRKWLCRQIPGTSSVVQ 263
 Qy 256 RNWKRPQSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
 | ||: :| :| |||| | ||:||:|||||:|||:|||||:
 Db 264 RKWKQ-----QQPVS---QPRGSGQQSKARI SAVAEEIKQIRARRKTARMLMVLLV 312
 Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
 ||:|||||:|||||:||| ||| ||| |||:|||||:|||||:|||||:
 Db 313 FAICYLPISILNVLKRVFGMFTHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 11

AAR01328

ID AAR01328 PRELIMINARY; PRT; 460 AA.
 AC AAR01328;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-2b.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Randeva H.S.;
 RT "Cloning and Characterization of the Mouse Type-2b Orexin Receptor
 RT Subtype (OX2bR).";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY336085; AAR01328.1; -.
 KW Receptor.
 SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

Query Match 69.0%; Score 1343.5; DB 2; Length 460;
 Best Local Similarity 71.7%; Pred. No. 1.6e-82;
 Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

Qy 17 SREPSPVPPDYED-EFLRYLWRDYLKPQYEWVLIAAYVAVFVVALGVNTLVCLAVWRNH 75
 :|| | ||:| |||||||:||:||:||||| |: |||||||:|| ||:||:||:
 Db 24 TQEPEFLNPTDYDDEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83
 Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPAVLVDITESWLFGHALCKVIPYLQAVSVSVAL 135
 |||||:|||||:|||||:| || :|||||:|| || :|||||:|| ||:||:
 Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVAL 143
 Qy 136 TLSFIALDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPPELANR 195
 ||| |||||||:|||||:||| ||: ||| |||:||| |||:|||:
 Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNSTIVVIWIVSCIIMIPQAIVMECSSMLPGLANK 203
 Qy 196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKWLGRQIPGTTSLV 255
 | ||:|||| | ::|||:|| |||:|||:||| || :|| ||||||| |||||:| :
 Db 204 TTLFTVCDEHWGGEVYPKMYHICFLVTYMAPLCLMILAYLQIFRKWLCRQIPGTSSVVQ 263

Qy 256 RNWKRPSDLQGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRTAKMLMVLLV 306
 | ||: :| :| |||| | ||:||:|||||:|||||||
 Db 264 RKWKQ-----QQPVS---QPRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLV 312
 ||:|||||:||||||| ||| ||| |||||||:|||||||
 Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
 ||:|||||:||||||| ||| ||| |||||||:|||||||
 Db 313 FAICYLPISILNVLKRVFGMFTHTEDRETIVYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 12

AAR11293

ID AAR11293 PRELIMINARY; PRT; 460 AA.
 AC AAR11293;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-2b.
 GN MOXR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Randeva H.S.;
 RT "Genomic structure analysis of the Mus musculus orexin type-2 (MOXR2) gene.";
 RT Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY339383; AAR11293.1; JOINED.
 DR EMBL; AY339384; AAR11293.1; JOINED.
 DR EMBL; AY339385; AAR11293.1; JOINED.
 DR EMBL; AY339386; AAR11293.1; JOINED.
 DR EMBL; AY339387; AAR11293.1; JOINED.
 DR EMBL; AY339388; AAR11293.1; JOINED.
 DR EMBL; AY339389; AAR11293.1; JOINED.
 DR EMBL; AY339390; AAR11293.1; -.
 KW Receptor.
 SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

Query Match 69.0%; Score 1343.5; DB 2; Length 460;
 Best Local Similarity 71.7%; Pred. No. 1.6e-82;
 Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

Qy 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVALVGNTLVCLAVWRNH 75
 ::|| | ||:| |||||||:||:||:||||| |: |||||||:|| | ||:||:|| | |||:
 Db 24 TQEPMFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVALIGNVLVCVAVWKNH 83
 |||||||:|||:||| | |||:||:||||| | || :||||| |||:|||:
 Qy 76 HMRTVTNYFIVNLSLADVLVTATCLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL 135
 |||:|||:|||:||| | |||:||:||||| | || :||||| |||:|||:
 Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVAL 143
 |||:|||:|||:||| | ||:||| | ||:||| |||:|||:
 Qy 136 TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAMECSSVLPPELANR 195
 |||:|||:|||:||| | ||:||| | ||:||| |||:|||:
 Db 144 TLSCLIALDRWYAICHPLMFKSTAKRARNNSIVVIWIVSCIIMIPQAIVMECSSMLPGLANK 203

Qy	196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTT SALV 255 : :: : : : : : :
Db	204 TTLFTVCDEHWGGEVYPKMYHICFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSV VQ 263
Qy	256 RNWKRPSDLQGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306 : : : : : : :
Db	264 RKWKQ-----QQPVS---QPRGSGQQSKARI SAVAEEIKQIRARRKTARMLMVLLV 312
Qy	307 FALCYLPISVLNVLKRVFGMFQASDREAVYACFTFSHLVYANSAANPIIYNFLSG 363 : : : : :
Db	313 FAICYLPISILNVLKRVFGMFHTEDRETVYAWFTFSHLVYANSAANPIIYNFLSG 369

RESULT 13

OX2R_RAT

ID OX2R_RAT STANDARD; PRT; 460 AA.
 AC P56719;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
 GN Name=Hcrtr2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98150861; PubMed=9491897;
 RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
 RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
 RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
 RA McNulty D.E., Liu W.-S., Terrell J.A., Elshourbagy N.A., Bergsma D.J.,
 RA Yanagisawa M.;
 RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
 RT and G protein-coupled receptors that regulate feeding behavior.";
 RL Cell 92:573-585(1998).
 RN [2]
 RP REVIEW.
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
 RA Hungs M., Mignot E.;
 RT "Hypocretin/orexin, sleep and narcolepsy.";
 RL Bioessays 23:397-408(2001).
 RN [3]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in the brain in the cerebral cortex,
 CC septal nuclei, hippocampus, medial thalamic groups, dorsal and
 CC median raphe nuclei, and many hypothalamic nuclei including the

CC tuberomammillary nucleus, dorsomedial hypothalamus,
 CC paraventricular hypothalamic nucleus, and ventral premammillary
 CC nucleus. Not detected in the spleen, lung, liver, skeletal muscle,
 CC kidney and testis. Orexin receptor mRNA expression has also been
 CC reported in the adrenal gland, enteric nervous system, and
 CC pancreas.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF041246; AAC40042.1; - .
 DR RGD; 2788; Hcrtr2.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 460 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 460 AA; 52489 MW; 3B44E3D82F8B85D5 CRC64;

 Query Match 69.0%; Score 1342.5; DB 1; Length 460;
 Best Local Similarity 72.0%; Pred. No. 1.8e-82;
 Matches 257; Conservative 37; Mismatches 42; Indels 21; Gaps 4;

 QY 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
 ::|| | ||:| |||||||:||:||:|||||| |: ||||||:|| ||:||:|||:
 Db 24 TQEPLNPTDYDDEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

 QY 76 HMRTVTNYFIVNLSLADVLVTAICLCPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL 135

Db	84	HMRTVTNYFIVNLSADVLVTITCLPATLVDITETWFFGQSLCKVIPYLQTVSVSVAL	143
Qy	136	TLSFIALDRWYAICHPLLKSTARRARGSILGIWAVSLAIMVPQAAMECSSVLP ELANR	195
Db	144	TLSCIALDRWYAICHPLMFKSTAKRARNSTIVVIWVSCIIMI PQAIIVMERSSMLPGANK	203
Qy	196	TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQI FRKLWGRQIPGTTSALV	255
Db	204	TTLFTVCDERWGGEVYPKMYHICFFLVTYMAPLCLMV LAYLQI FRKLWCRQIPGTSSVVQ	263
Qy	256	RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQM RARRKTAKMLMVLLV	306
Db	264	RWKQPP-----QPVS---QPRGSGQQSKARI SAVAAEIKQIRARRKTARMLMVLLV	312
Qy	307	FALCYLPISVNLVLRVFGMFRQASDRE AVYACFTFSHWLVYANSAANPIIYNFLSG	363
Db	313	FAICYLPISILNVLRVFGMFTHTEDRET VYAWFTFSHWLVYANSAANPIIYNFLSG	369

RESULT 14

OX2R HUMAN

ID - OX2R_HUMAN STANDARD; PRT; 444 AA.
AC 043614;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
GN Name=HCRT2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98150861; PubMed=9491897;
RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA McNulty D.E., Liu W.-S., Terrell J.A., Elshourbagy N.A., Bergsma D.J.,
RA Yanagisawa M.;
RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT and G protein-coupled receptors that regulate feeding behavior.";
RL Cell 92:573-585(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21580342; PubMed=11723285;
RA Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,
RA Stefansson K., Gulcher J.R.;
RT "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";
RL Neurology 57:1896-1899(2001).
RN [3]
RP REVIEW.
RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
RA Hungs M., Mignot E.;
RT "Hypocretin/orexin, sleep and narcolepsy.";
RL Bioessays 23:397-408(2001).

RN [4]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF041245; AAC39602.1; -.
 DR EMBL; AY062031; AAL47215.1; -.
 DR Genew; HGNC:4849; HCRTR2.
 DR MIM; 602393; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0008188; F:neuropeptide receptor activity; TAS.
 DR GO; GO:0007631; P:feeding behavior; TAS.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 444 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 444 AA; 50680 MW; CA0669F0D4224C65 CRC64;
 Query Match 68.9%; Score 1341.5; DB 1; Length 444;
 Best Local Similarity 71.4%; Pred. No. 2.1e-82;
 Matches 255; Conservative 35; Mismatches 46; Indels 21; Gaps 3;

 Qy 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
 ::|| | ||:| |||||||:||:||:||||| :|:|||||:|| |||:|||:
 Db 24 TQEFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

 Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL 135
 |||||||:|||||:|||||:|||:|||:|||:|||:|||:|||:
 Db 84 HMRTVTNYFIVNLSLADVLVITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVAL 143

 Qy 136 TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPANR 195
 ||| |||||||:|||:|||:|||:|||:|||:
 Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNNSIVIWIVSCTIMIPQAIVMECSTVFPGLANK 203

 Qy 196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSSALV 255
 | ||:|||||:|||:|||:|||:|||:|||:|||:
 Db 204 TTLFTVCDERWGGEIYPKMYHICFFLVYMAPLCLMVAYLQIFRKLWCRQIPGTSSVVQ 263

 Qy 256 RNWKRPSDLQGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
 | || | ||| | |||:|||:|||:|||:|||:
 Db 264 RKWK-----PLQPVSQPRGPQPTKSRMSAVAEIKQIRARRKTARMLMVLLV 312

 Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
 ||:|||||:|||||:|||:|||:
 Db 313 FAICYLPISILNVLKRVFGMFAHTEDRETVDYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 15

AAG28021

ID AAG28021 PRELIMINARY; PRT; 444 AA.
 AC AAG28021;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypocretin receptor-2.
 GN HCRTTR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20429525; PubMed=10973318;
 RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,
 RA Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,
 RA Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,
 RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;
 RT "A mutation in a case of early onset narcolepsy and a generalized
 absence of hypocretin peptides in human narcoleptic brains.";
 RL Nat. Med. 6:991-997(2000).
 DR EMBL; AF202091; AAG28021.1; -.
 DR EMBL; AF202085; AAG28021.1; JOINED.
 DR EMBL; AF202086; AAG28021.1; JOINED.

DR EMBL; AF202087; AAG28021.1; JOINED.
 DR EMBL; AF202088; AAG28021.1; JOINED.
 DR EMBL; AF202089; AAG28021.1; JOINED.
 DR EMBL; AF202090; AAG28021.1; JOINED.
 KW Receptor.
 SQ SEQUENCE 444 AA; 50680 MW; CA0669F0D4224C65 CRC64;

 Query Match 68.9%; Score 1341.5; DB 2; Length 444;
 Best Local Similarity 71.4%; Pred. No. 2.1e-82;
 Matches 255; Conservative 35; Mismatches 46; Indels 21; Gaps 3;

 Qy 17 SREPSPVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
 ::|| | ||:| |||||||:||:||:||||| :|:||||||:|| |||:||:|| |||:
 Db 24 TQEPEFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCAVWKNH 83

 Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAL 135
 |||||||:|||||:|| |||:||:|||||:|| || :|||||||:|| |||:
 Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLUVVDITETWFFGQSLCKVIPYLQTVSVSVAL 143

 Qy 136 TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAVMECSSVLPLEANR 195
 ||| |||||||:|||:||| ||:|| || |||:||| |||:
 Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNIVIIWIVSCIIMIPQAIVMECSTVFPGLANK 203

 Qy 196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
 | ||:||||| :|||:|| |||:|||:|| || :|| |||:||| |||:
 Db 204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVAYLQIFRKLWCRQIPGTSSVVQ 263

 Qy 256 RNWKRPSDLQGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
 | || | ||| | ||| | ||| | |||:|||:|||:|||:|||:
 Db 264 RKWK-----PLQPVSQPRGPQOPTKSRSMSAAEIKQIRARRKTARMLMVLLV 312

 Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
 ||:|||||:|||||:||| ||| ||| |||:|||:|||:|||:
 Db 313 FAICYLPISILNVLKRVFGMFAHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

Search completed: October 14, 2004, 10:55:50
 Job time : 98.6261 secs